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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 13.8519 Seconds  
(without alignments)  
152,738 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	122	100.0	540 2 A26950	groEL2 protein - M
2	122	100.0	540 2 A43509	65k antigen mbaa -
3	122	100.0	540 2 C41325	heat shock protein
4	122	100.0	541 2 S40245	heat shock protein
5	122	100.0	541 2 T44725	chaperonin 60k (im
6	122	100.0	588 2 A25902	65k antigen - Myco
7	112	91.8	538 2 H72367	groEL protein - Th
8	107	87.7	540 2 B41325	heat shock protein
9	107	87.7	541 2 T35591	chaperonin cpn60 -
10	103	84.4	538 2 Q01195	heat shock protein
11	103	84.4	539 2 B49855	heat shock protein
12	103	84.4	541 2 S72614	chaperonin 60 - Th
13	103	84.4	542 2 AC1704	class I heat-shock
14	103	84.4	542 2 AD1333	class I heat-shock
15	103	84.4	543 2 B41872	heat shock protein
16	103	84.4	543 2 F97232	chaperonin groEL,
17	103	84.4	544 2 JC5130	heat shock protein
18	103	84.4	544 2 B41884	58k heat shock pro
19	103	84.4	544 2 JC6063	chaperonin groEL -
20	103	84.4	544 2 B83720	class I heat-shock
21	102	83.6	543 2 S70013	chaperonin-like pr
22	101	82.8	528 2 S73270	chaperonin, 60k -
23	101	82.8	541 2 T06829	chaperonin groEL -
24	101	82.8	544 2 A43263	chaperonin groEL
25	101	82.8	546 2 S34938	heat shock protein
26	100	82.0	541 2 B68249	chaperonin groEL h
27	100	82.0	544 1 BYRCL	chaperonin groEL
28	100	82.0	546 2 B47073	chaperonin groEL -
29	99	81.1	539 2 S22342	chaperonin HSP60 -

30	99	81.1	542 2 JN0661	heat shock protein
31	99	81.1	542 2 S32106	groEL protein - La
32	99	81.1	542 2 B86674	60 KD chaperonin
33	98	80.3	540 2 G95222	chaperonin, 60 kDa
34	98	80.3	540 2 H98086	chaperonin groEL
35	98	80.3	544 2 B82048	chaperonin, 60 kD
36	98	80.3	547 2 JC4519	heat-shock protein
37	98	80.3	547 2 B43606	heat shock protein
38	98	80.3	547 2 B83098	chaperonin groEL
39	98	80.3	548 1 BYRCL	chaperonin groEL -
40	98	80.3	548 2 D91269	chaperonin groEL
41	98	80.3	548 2 G75439	groEL protein - De
42	98	80.3	548 2 B86110	hypothetical prote
43	98	80.3	548 2 A51045	groEL protein (imp
44	98	80.3	550 2 A41468	60k heat shock pro
45	98	80.3	552 2 S39765	chaperonin 60 - Co

#### ALIGNMENTS

RESULT 1  
A26950  
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)  
N/Alternate names: 65k antigen  
C/Species: Mycobacterium tuberculosis  
C/Date: 02-Jun-1998 #sequence\_revision 02-Jun-1998 #text\_change 20-Jun-2000  
C/Accession: A26950; A70830  
R/Shimnick, T.M.  
J. Bacteriol. 169, 1080-1088, 1987  
A/Title: The 65-Kilodalton antigen of Mycobacterium tuberculosis.  
A/Reference number: A26950; MUID:87137260; PMID:3029018  
A/Accession: A26950  
A/Molecule type: DNA  
A/Residues: 1-540 <SH1>  
A/Cross-references: GB:M5467; NID:g149999; PIDN:AAA89232.1; PID:g150000  
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, I.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A/Reference number: A70500; MUID:98295987; PMID:9634230  
A/Accession: A70830  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Residues: 1-540 <COL>  
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17397.1; PID:g29095;  
C/Experimental source: strain H37RV  
C/Genetics:  
A/Gene: groEL2; Rv0440  
C/Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;  
Best local similarity 100.0%; Pred. No. 9.1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAPITINDG 22  
DB 31 GPKGRNVVLEKKMGAPITINDG 52

RESULT 2  
A43509  
65k antigen mbaa - Mycobacterium bovis  
C/Species: Mycobacterium bovis  
C/Date: 28-Oct-1992 #sequence\_revision 28-Oct-1992 #text\_change 26-Aug-1999  
C/Accession: A43509  
R/Thole, J.E.R.; Keulen, W.J.; Kolj, A.H.J.; Groothuis, D.G.; Berauld, L.G.; Tiesjema, I. Infect. Immun. 55, 1466-1475, 1987  
A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton  
A/Reference number: A43509; MUID:8719315; PMID:3553003  
A/Accession: A43509

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <THO>  
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GPKGRNVLEKKWGAPITNDG 22  
Db 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 3  
C41325  
heat shock protein 56 - Streptomyces albus  
N/Alternate names: heat shock protein groEL homolog 2  
C/Species: Streptomyces albus  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 26-Aug-1999  
C/Accession: C41325  
R/Mazodier, P.; Gujiljemi, G.; Davies, J.; Thompson, C.J.  
J. Bacteriol. 173, 7382-7386, 1991  
A/Title: Characterization of the groEL-like genes in Streptomyces albus.  
A/Reference number: A41325; MUID:92041639; PMID:1682304  
A/Accession: C41325  
A:Molecule type: DNA  
A:Residues: 1-540 <MAZ>  
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294  
C/Genetics:  
A:Gene: groEL2  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GPKGRNVLEKKWGAPITNDG 22  
Db 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 4  
S40245  
heat shock protein 65 - Mycobacterium paratuberculosis  
C/Species: Mycobacterium paratuberculosis  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
C/Accession: S40245  
R/Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdoso, R.  
submitted to the EMBL Data Library, August 1993  
A/Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.  
A/Reference number: S40245  
A/Accession: S40245  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <COL>  
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVLEKKWGAPITNDG 22  
Db 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 5  
T44725  
chaperonin 60K [imported] - Mycobacterium leprae  
N/Alternate names: heat shock protein GroEL-2

C/Species: Mycobacterium leprae  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C/Accession: T44725  
R/James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A/Reference number: Z22831  
A/Accession: T44725  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-541 <JAM>  
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1  
A:Experimental source: cosmid B1450  
C/Genetics:  
A:Gene: groEL-2  
C:Superfamily: chaperonin groEL  
C/Keywords: molecular chaperone

Query Match 100.0%; Score 122; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVLEKKWGAPITNDG 22  
Db 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 6  
A25902  
65K antigen - Mycobacterium leprae  
C/Species: Mycobacterium leprae  
C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997  
C/Accession: A25902  
R/Mehra, V.; Sweetser, D.; Young, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986  
A/Title: Efficient mapping of protein antigenic determinants.  
A/Reference number: A25902; MUID:86313701; PMID:2428046  
A/Accession: A25902  
A:Molecule type: DNA  
A:Residues: 1-588 <MEH>  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVLEKKWGAPITNDG 22  
Db 78 GPKGRNVLEKKWGAPITNDG 99

RESULT 7  
H72367  
groEL protein - Thermotoga maritima (strain MSB8)  
C/Species: Thermotoga maritima  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C/Accession: H72367  
R/Nelson, K.R.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.  
Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A/Reference number: A72200; MUID:99287316; PMID:10360571  
A/Accession: H72367  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-538 <ARN>  
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AAD35591.1; PID:g4981015  
A:Experimental source: strain MSB8  
C/Genetics:  
A:Gene: TM0506  
C:Superfamily: chaperonin groEL

Query Match 91.8%; Score 112; DB 2; Length 538;

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# OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 9.37037 Seconds  
(without alignments)  
110.411 Million cell updates/sec

Title: US-09-847-637B-1  
Perfect score: 122  
Sequence: 1 GPGKGRVIVLEKKWGAPITNDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	476	1	CH62_STRLI
2	122	100.0	539	1	CH60_TSTRY
3	122	100.0	539	1	CH62_MYCTU
4	122	100.0	539	1	CH62_MYCTU
5	122	100.0	540	1	CH60_MYCPA
6	122	100.0	540	1	CH60_MYCPA
7	122	100.0	540	1	CH62_MYCTE
8	122	100.0	541	1	CH60_COREQ
9	122	100.0	541	1	CH60_NOCPA
10	122	100.0	541	1	CH60_STRCO
11	122	100.0	542	1	CH60_NOCAS
12	117	95.9	544	1	CH60_PROAC
13	116	95.1	547	1	CH62_COREF
14	116	95.1	548	1	CH62_COREG
15	114	93.4	540	1	CH60_TROWT
16	112	91.8	538	1	CH60_THEMA
17	112	91.8	538	1	CH60_THEMA
18	107	87.7	539	1	CH61_STRLA
19	107	87.7	540	1	CH61_STRCO
20	105	86.1	537	1	CH60_PARDN
21	105	86.1	537	1	CH60_PARDN
22	104	85.2	541	1	CH60_GARVA
23	104	85.2	541	1	CH60_BIFLO
24	104	85.2	541	1	CH60_BIFLO
25	103	84.4	538	1	CH60_BACPI
26	103	84.4	539	1	CH60_BACPI
27	103	84.4	539	1	CH60_BACPI
28	103	84.4	540	1	CH60_THBR
29	103	84.4	542	1	CH60_LISIN
30	103	84.4	542	1	CH60_LISIN
31	103	84.4	543	1	CH60_BACSU
32	103	84.4	543	1	CH60_BACSU
33	103	84.4	543	1	CH60_BACSU

34	103	84.4	544	1	CH60_BACHD	O50305 bacillus ha
35	102	83.6	540	1	CH60_RHOKR	O9KCA9 rhodotherm
36	102	83.6	540	1	CH60_THERN	O85577 thermoaer
37	102	83.6	543	1	CH60_ANASL	O9AMJ8 anabaena sp
38	102	83.6	543	1	CH60_LACJO	O9KJ23 lactobacill
39	102	83.6	543	1	CH62_SYNEL	O57002 synechococc
40	101	82.8	528	1	CH60_PORPU	P51349 porphyra pu
41	101	82.8	538	1	CH60_SCAIO	O9EY76 scardovia i
42	101	82.8	541	1	CH60_CVAPA	O37757 cyanophora
43	101	82.8	544	1	CH61_ANASP	O8Y928 anabaena sp
44	101	82.8	544	1	CH61_SYNYU	O50323 synechococc
45	101	82.8	545	1	CH60_SYNEL	O8AMd4 synechococc

## ALIGNMENTS

RESULT 1  
ID CH62\_STRLI STANDARD; PRT; 476 AA.  
AC O31658;  
DT 16-OCT-2001 (Rel. 40; Created)  
DT 16-OCT-2001 (Rel. 40; Last sequence update)  
DT 28-FEB-2003 (Rel. 41; Last annotation update)  
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).  
GN GROEL2 OR GROEL2.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycesetaceae; Streptomyces.  
OX NCBI\_TaxID:1916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TX21;  
RX MEDLINE=98048481; PubMed=9387235;  
RA de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.,  
RA Mellado R.P.,  
RT "Streptomyces lividans groEL1 and groEL2 genes";  
RL Microbiology 143:3563-3571 (1997).  
CC -1- FUNCTION: Prevents misfolding and promotes the refolding and  
proper assembly of unfolded polypeptides generated under stress  
conditions (By similarity).  
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of  
7 subunits (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
EMBL: X95971; CA65226.1; -.  
DR HSMAP; P06139; IGRU.  
DR HSMAP; MF 00600; atypical; 1.  
DR InterPro; IPR001844; Chaperin Cpn60.  
DR InterPro; IPR002423; Cpn60/TCP-1.  
DR Pfam; PF00118; Cpn60\_TCP1; 1.  
DR PRINTS; PR002984; CHAPERONIN60.  
DR PRINTS; PR00304; TCOMPLEXTCP1.  
DR PROSITE; PS00296; CHAPERONIN60; 1.  
KW Chaperone; ATP-binding; Multigene family.  
FT INIT MET 0  
SQ  
SEQUENCE 476 AA; 50529 MW; 760F81793F4FED4D CRC64;  
Query Match 100.0%; Score 122; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 8.9e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GPGKGRVIVLEKKWGAPITNDG 22  
|||||

DB 30 GPKGRNVLEKKMGAPITINDG 51

RESULT 2

CH60 TSUTY STANDARD; PRT; 539 AA.

AC P97086;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (heat shock protein 60);

GN GROEL OR GROEL OR HSP60.

OS Tsukamurella tyrosinosa tyrosinosa.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Tsukamurellaceae; Tsukamurella.

OX NCBI\_TaxID=57704;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IMTB D-1411;

RA Zimmermann O., Pinkenburg O., Koechel H.G.;

RT "Tsukamurella tyrosinosa sp. nov. hsp60 gene for heat shock protein 60.";

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.

CC -----

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CC -----

CC EMBL; U90204; AAB49990.1; -.

DR HSP60; P06139; 1GRL.

DR HAMAP; MF 00600; -; 1.

DR InterPro: IPR001844; Chaperonin Cpn60.

DR InterPro: IPR002423; Cpn60/TCP1.

DR Pfam; PF00118; Cpn60\_TCP1.1.

DR PRINTS; PR00296; CHAPERONIN60.

DR PRINTS; PR00304; TCOMPLEXTCP1.

DR PROSITE; PS00236; CHAPERONINS\_CPN60; 1.

KW Chaperone; ATP-binding.

SO SEQUENCE 539 AA; 56137 MW; 6353514830C9B662 CRC64;

Query Match 100.0%; Score 122; DB 1; Length 539;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAPITINDG 22

DB 31 GPKGRNVLEKKMGAPITINDG 52

RESULT 3

CH62 MYCTU STANDARD; PRT; 539 AA.

ID P06806; Q48920; Q48931;

AC P06806; Q48920; Q48931;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (Heat shock protein 65) (Cell wall protein A) (Antigen A).

GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.

OS Mycobacterium tuberculosis, and Mycobacterium bovis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1773, 1765;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=Brdmann;

RX MEDLINE=87137260; PubMed=3029018;

RA Shimnick T.M.;

RT "The 65-kilodalton antigen of Mycobacterium tuberculosis.";

RL J. Bacteriol. 169:1080-1088 (1987).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;

RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RL Nature 393:537-544 (1998).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishel W.;

RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=8719315; PubMed=3553003;

RA Thole J.B.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Bernald L.G., Tiesjema R.H., van Embden J.D.A.;

RT "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of Mycobacterium bovis BCG expressed in Escherichia coli K-12.";

RL Infect. Immun. 55:1466-1475 (1987).

RN [5]

RP SEQUENCE OF 45-195 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;

RA Ros C., Belak K.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE OF 63-182 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMC 410, and TMC 1024;

RX MEDLINE=95150784; PubMed=7848059;

RA Kapur V., Li L.L., Hamrick M.R., Pilkytis B.B., Shimnick T.M., Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Clarridge J.E., Kreiswirth B.N., Musser J.M.;

RA "Rapid Mycobacterium species assignment and unambiguous identification of mutations associated with antimicrobial resistance in Mycobacterium tuberculosis by automated DNA sequencing.";

RL Arch. Pathol. Lab. Med. 119:131-138 (1995).

RN [7]

RP SEQUENCE OF 64-177 FROM N.A.

RC SPECIES=M.tuberculosis;

RX MEDLINE=95214306; PubMed=7699930;

RA Hidaka E., Ueno I., Kawakami Y., Furutawari C., Furinata K., Katsuyama T.;

RA "Detection and identification of mycobacteria by PCR-RFLP method.";

RL Rinsho Byori 43:155-161 (1995).

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 35.4444 Seconds  
(without alignments)  
160.171 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioplasmid:\*
- 17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	59	2	Q9EMD1 streptomycin
2	122	100.0	61	2	Q9EUB7 streptomycin
3	122	100.0	539	2	P97086 streptomycin
4	122	100.0	540	2	Q9AFN5 streptomycin
5	122	100.0	541	2	Q93Q12 streptomycin
6	122	100.0	541	2	Q9AFN6 streptomycin
7	122	100.0	541	2	Q9GWI1 streptomycin
8	122	100.0	542	2	Q9APC5 streptomycin
9	122	100.0	548	2	Q9GAR8 streptomycin
10	122	100.0	548	2	Q9GAR8 streptomycin
11	122	100.0	548	2	Q9G923 streptomycin
12	122	100.0	548	2	Q9G8X0 streptomycin
13	122	100.0	549	2	Q9GAR9 streptomycin
14	122	100.0	533	2	Q9FDS2 streptomycin
15	116	95.1	547	16	Q8CT22 streptomycin
16	116	95.1	548	16	Q8NM64 streptomycin

17	105	86.1	537	2	Q9K171	Q9K171 parascardov
18	105	86.1	541	2	Q9K157	Q9K157 gaidnerella
19	104	85.2	537	2	Q9JMT8	Q9JMT8 bifidobacte
20	104	85.2	541	16	Q9G879	Q9G879 bifidobacte
21	104	85.2	582	2	Q9REU4	Q9REU4 bifidobacte
22	103	84.4	539	2	Q9RZV4	Q9RZV4 bacillus st
23	103	84.4	539	2	Q9RC20	Q9RC20 bacillus st
24	103	84.4	545	2	Q9GB95	Q9GB95 bacillus st
25	102	83.6	543	2	Q9AMJ8	Q9AMJ8 anabaena sp
26	101	82.8	538	2	Q9EY76	Q9EY76 scardovia i
27	101	82.8	545	16	Q9DMD4	Q9DMD4 synchococc
28	101	82.8	546	2	Q91198	Q91198 leptospira
29	100	82.0	543	2	Q9KZM2	Q9KZM2 thermus sp.
30	100	82.0	545	16	Q9CX13	Q9CX13 oceanobacil
31	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
32	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
33	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
34	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
35	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
36	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
37	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
38	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
39	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
40	98	80.3	191	2	Q9VUS2	Q9VUS2 secondary s
41	98	80.3	329	2	Q9EWA9	Q9EWA9 serratia ma
42	98	80.3	329	2	Q9EWA8	Q9EWA8 serratia ma
43	98	80.3	329	2	Q9EXM7	Q9EXM7 enterobacte
44	98	80.3	329	2	Q9EXM5	Q9EXM5 enterobacte
45	98	80.3	329	2	Q9F2H2	Q9F2H2 serratia ma

## ALIGNMENTS

### RESULT 1

Q9EMD1	PRELIMINARY;	PRT;	59 AA.
AC	Q9EMD1		
ID	Q9EMD1		
AD	Q9EMD1		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Heat-shock protein (Fragment).		
GN	GROEL2.		
OS	Streptomyces coelicolor.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Streptomycineae; Streptomycetaceae; Streptomycetes.		
OX	NCBI_TaxID=1902;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=J802;		
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;		
RT	"A cold-shock-like gene with pleiotropic effects on streptomycetes.		
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AJ250536; CAC19351.1; -.		
DR	HSSP; P06139; IAO.		
DR	InterPro; IPR02423; Cpn60/TCP-1.		
DR	Pfam; PF00118; cpn60 TCP1.1		
DR	PRINTS; PR00304; TCOMPLXTCPL.		
KW	ATP-binding; Chaperone.		
FT	NON TER		
SQ	SEQUENCE 59 AA; 6407 MW; E7B2419B7DE68FA CRC64;		

Query Match 100.0%; Score 122; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. NO. 9.8e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPKGRNVVLEKKMGAPITINDG 22
Db	31	GPKGRNVVLEKKMGAPITINDG 52
RESULT 2		

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Q9EUR7          PRELIMINARY;          PRT;          61 AA.
ID Q9EUR7
AC Q9EUR7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Heat-shock protein (Fragment).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costra O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; cpn60_TCF1.1.
DR PRINTS; PR00304; TCOMPLEXTCPL.
KW ATP-binding; Chaperone.
FT NON TER
SQ SEQUENCE 61 AA; 6645 MW; D20095F4199B7CA CRC64;

Query Match          100.0%; Score 122; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTINDG 22
DB 31 GPKGRNVLEKKWGAPTTINDG 52

RESULT 3
P97086          PRELIMINARY;          PRT;          539 AA.
ID P97086
AC P97086;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella tyrosinosevens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosevens sp. nov. hsp60 gene for heat shock
RT protein 60."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaprin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; cpn60_TCF1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49BF7C CRC64;

Query Match          100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTINDG 22
DB 31 GPKGRNVLEKKWGAPTTINDG 52

RESULT 4
Q9AFAS          PRELIMINARY;          PRT;          540 AA.
ID Q9AFAS
AC Q9AFAS;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaprin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; cpn60_TCF1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49BF7C CRC64;

Query Match          100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTINDG 22
DB 31 GPKGRNVLEKKWGAPTTINDG 52

RESULT 5
Q93012          PRELIMINARY;          PRT;          541 AA.
ID Q93012
AC Q93012;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match          100.0%; Score 122; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTINDG 22
DB 31 GPKGRNVLEKKWGAPTTINDG 52

RESULT 4
Q9AFAS          PRELIMINARY;          PRT;          540 AA.
ID Q9AFAS
AC Q9AFAS;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaprin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; cpn60_TCF1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49BF7C CRC64;

Query Match          100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTINDG 22
DB 31 GPKGRNVLEKKWGAPTTINDG 52

RESULT 5
Q93012          PRELIMINARY;          PRT;          541 AA.
ID Q93012
AC Q93012;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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1	122	100.0	22	21	AAV93328	Amino acid sequen
2	122	100.0	25	19	AAW60145	M. vaccae antigen
3	122	100.0	215	20	AAV14892	Amino acid sequen
4	122	100.0	215	23	ABW73468	M. vaccae GroEL hom
5	122	100.0	295	22	AAW31645	Amino acid sequen
6	122	100.0	523	19	AAW60144	M. vaccae antigen
7	122	100.0	523	20	AAV14891	Amino acid sequen
8	122	100.0	523	23	ABW73467	M. vaccae GroEL hom
9	122	100.0	539	20	AAV23919	Amino acid sequen

[illegible]

PT especially arthritis .

XX Claim 1; Page 7; 58pp; English.  
 XX  
 XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of *Mycobacterium tuberculosis*. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX  
 SQ Sequence 22 AA;  
 Query Match 100.0%; Score 122; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-13;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAPITNDG 22  
 DB 1 GPKGRNVLEKKWGAPITNDG 22  
 RESULT 2  
 AAM60145  
 ID AAM60145 standard; protein; 215 AA.  
 XX  
 AC AAM60145;  
 XX  
 DT 25-AUG-1998 (first entry)  
 XX  
 DE M. vaccae antigen GV-27A sequence.  
 XX  
 KM *Mycobacterium vaccae*; antigen; therapy; prevention; cytokine production;  
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KM *Mycobacterium vaccae*; vaccine; cancer.  
 XX  
 OS *Mycobacterium vaccae*.  
 XX  
 PN WO9808542-A2.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 28-AUG-1997; 97WO-NZ00105.  
 XX  
 PR 12-JUN-1997; 97US-0873970.  
 PR 29-AUG-1996; 96US-0705347.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP.  
 XX  
 PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P,  
 PI Visser E;  
 XX  
 DR WPI, 1998-216926/19.  
 DR N-PSDB; AAV34609.  
 XX  
 PT *Mycobacterium vaccae* polypeptides - used to develop products for use  
 PT in detection, therapy and prevention of *Mycobacterium tuberculosis* or  
 PT as immune response enhancers  
 XX  
 Claim 48; Pages 117-118; 153pp; English.  
 XX  
 CC This represents a *Mycobacterium vaccae* antigen GV-27A. The invention  
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of  
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an  
 CC immune response in patients previously exposed to a *Mycobacterium*. Such  
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific  
 CC immune response. The methods and products can be used for the detection,  
 CC treatment and prevention of infectious diseases caused by *Mycobacterium*  
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
 CC the ability to induce cell proliferation and cytokine production (e.g.  
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,  
 CC B cells, or macrophages. They can be used for enhancing immune responses  
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

SQ Sequence 215 AA;  
 Query Match 100.0%; Score 122; DB 19; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-12;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAPITNDG 22  
 DB 31 GPKGRNVLEKKWGAPITNDG 52  
 RESULT 3  
 AAY14892  
 ID AAY14892 standard; protein; 215 AA.  
 XX  
 AC AAY14892;  
 XX  
 DT 25-OCT-1999 (first entry)  
 XX  
 DE Amino acid sequence of M. vaccae antigen GV-27A.  
 XX  
 KM *Mycobacterium vaccae* protein; antigen; T cell activation; cytokine;  
 KM dendritic cell maturation; infectious disease; immune disorder; cancer;  
 KM respiratory system; *Mycobacterium tuberculosis*; allergy; tuberculosis;  
 KM leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;  
 KM dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;  
 KM squamous cell carcinoma; melanoma.  
 XX  
 OS *Mycobacterium vaccae*.  
 XX  
 PN WO9932634-A2.  
 XX  
 PD 01-JUL-1999.  
 XX  
 PF 23-DEC-1998; 98WO-NZ00189.  
 XX  
 PR 04-DEC-1998; 98US-0205426.  
 PR 23-DEC-1997; 97US-0996624.  
 PR 23-DEC-1997; 97US-0997080.  
 PR 23-DEC-1997; 97US-0997362.  
 PR 11-JUN-1998; 98US-0095855.  
 PR 17-SEP-1998; 98US-0156181.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;  
 PI N-PSDB; AAZ11344.  
 XX  
 DR WPI, 1999-430163/36.  
 DR N-PSDB; AAZ11344.  
 XX  
 PT Enhancing immune response to an antigen  
 XX  
 Example 14; Page 191-192; 243pp; English.  
 XX  
 CC The invention provides heat-killed *Mycobacterium vaccae*, or recombinant  
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate  
 CC T cells and natural killer cells, to stimulate the production of  
 CC cytokines; to enhance the expression of co-stimulatory molecules on  
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation  
 CC and function. The proteins can be expressed by standard recombinant  
 CC methodology. Pharmaceutical compositions comprising the proteins or  
 CC nucleic acid sequences encoding the proteins can be used for the  
 CC treatment, prevention, and detection of disorders including infectious  
 CC diseases, immune disorders and cancer. In particular, the compounds and  
 CC methods are used for treatment of diseases of the respiratory system,  
 CC such as *Mycobacterium tuberculosis*, asthma, allergies, tuberculosis,  
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as  
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,  
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell  
 CC carcinoma, and melanoma.  
 XX  
 SQ Sequence 215 AA;

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 30, 2003, 16:09:39 ; Search time 30.1481 Seconds  
(without alignments)  
145.229 Million cell updates/sec

Title: US-09-847-637b-1  
Sequence: 1 GPKGRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	22	10	US-09-847-637b-1
2	122	100.0	215	11	US-09-880-505-117
3	122	100.0	215	12	US-10-205-979-41
4	122	100.0	215	14	US-10-051-643-117
5	122	100.0	295	15	US-10-267-311-33
6	122	100.0	523	11	US-09-880-505-114
7	122	100.0	523	14	US-10-051-643-114
8	122	100.0	540	10	US-09-847-637b-6
9	122	100.0	540	10	US-09-712-363-169
10	122	100.0	540	15	US-10-267-311-4
11	122	100.0	540	15	US-10-046-649-3
12	122	100.0	541	15	US-10-046-649-4
13	122	100.0	541	11	US-09-880-505-160
14	122	100.0	541	12	US-10-205-979-40
15	122	100.0	541	14	US-10-051-643-160

16	122	100.0	541	15	US-10-156-761-11465	Sequence 11465, A
17	122	100.0	576	12	US-10-369-493-8322	Sequence 8322, Ap
18	122	100.0	639	15	US-10-267-311-17	Sequence 17, Appl
19	122	100.0	648	15	US-10-267-311-29	Sequence 29, Appl
20	122	100.0	690	14	US-10-068-059-10	Sequence 10, Appl
21	122	100.0	709	14	US-10-068-059-8	Sequence 8, Appl
22	122	100.0	724	14	US-10-068-059-12	Sequence 12, Appl
23	122	100.0	746	14	US-10-068-059-6	Sequence 6, Appl
24	122	100.0	948	15	US-10-267-311-21	Sequence 21, Appl
25	116	95.1	538	10	US-09-738-626-6486	Sequence 6486, Ap
26	112	91.8	538	12	US-10-369-493-2950	Sequence 2950, Ap
27	107	87.7	544	15	US-10-156-761-12526	Sequence 12526, A
28	103	84.4	544	12	US-10-369-493-17132	Sequence 17132, A
29	103	84.4	544	12	US-10-369-493-23094	Sequence 23094, A
30	101	82.8	521	12	US-10-369-493-9597	Sequence 9597, Ap
31	101	82.8	544	12	US-10-369-493-15838	Sequence 15838, A
32	101	82.8	544	12	US-10-369-493-15468	Sequence 15468, A
33	101	82.8	544	12	US-10-369-493-16217	Sequence 16217, A
34	101	82.8	544	12	US-10-369-493-20276	Sequence 20276, A
35	100	82.0	544	12	US-10-369-493-20873	Sequence 20873, A
36	100	82.0	545	12	US-10-369-493-19756	Sequence 19756, A
37	99	81.1	547	12	US-10-369-493-10014	Sequence 10014, A
38	98	80.3	547	15	US-10-046-649-2	Sequence 2, Appl
39	98	80.3	548	11	US-09-415-849-1	Sequence 1, Appl
40	98	80.3	548	11	US-09-276-455-10	Sequence 10, Appl
41	98	80.3	548	12	US-10-369-493-513	Sequence 513, Appl
42	98	80.3	551	12	US-10-369-493-20184	Sequence 20184, A
43	98	80.3	641	15	US-10-267-311-51	Sequence 51, Appl
44	97	79.5	545	12	US-10-228-167A-2	Sequence 2, Appl
45	95	77.9	551	12	US-10-369-493-18994	Sequence 18994, A

## ALIGNMENTS

RESULT 1  
US-09-847-637b-1  
; Sequence 1, Application US/09847637B  
; Patent No. US20020150586A1  
; GENERAL INFORMATION:  
; APPLICANT: Niparstek, Yaakov  
; APPLICANT: Umanetsky, Rina  
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF  
; FILE REFERENCE: 13125-002001  
; CURRENT APPLICATION NUMBER: US/09/847, 637B  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: PCT/IL99/00595  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,213  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
; US-09-847-637b-1

Query Match 100.0%; Score 122; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.6e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAPITINDG 22  
|||||  
DB 1 GPKGRNVVLEKKMGAPITINDG 22  
|||||

RESULT 2  
US-09-880-505-117  
; Sequence 117, Application US/09880505

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Publication No. US20030007976A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c2
CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR FILING DATE: 1999-06-02
PRIOR FILING DATE: 1997-12-23
PRIOR APPLICATION NUMBER: US 08/997,080
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-09-880-505-117

Query Match      100.0%; Score 122; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 3
US-10-205-979-41
Sequence 41, Application US/10205979
Publication No. US20030147861A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Abernethy, Nevyn
TITLE OF INVENTION: Compounds and Methods for the Modulation
of Immune Responses
FILE REFERENCE: 11000.1063U
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-10-205-979-41

Query Match      100.0%; Score 122; DB 12; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 4
US-10-051-643-117
Sequence 117, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Diseases of the Respiratory
System using Mycobacterium vaccae
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FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-10-051-643-117

Query Match      100.0%; Score 122; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 5
US-10-267-311-33
Sequence 33, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-33

Query Match      100.0%; Score 122; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 5,7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 6
US-09-880-505-114
Sequence 114, Application US/09880505
Publication No. US20030007976A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c2
CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 15.4815 Seconds  
(without alignments)  
60.126 Million cell updates/sec

Title: US-09-847-637B-1  
Perfect score: 122  
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	122	100.0	215 2 US-08-997-362-117	Sequence 117, App
3	122	100.0	215 3 US-09-095-855-117	Sequence 117, App
4	122	100.0	215 4 US-09-324-542-117	Sequence 117, App
5	122	100.0	215 4 US-09-205-426-117	Sequence 117, App
6	122	100.0	295 4 US-09-613-303-33	Sequence 114, App
7	122	100.0	523 2 US-08-997-080-114	Sequence 114, App
8	122	100.0	523 2 US-08-997-362-114	Sequence 114, App
9	122	100.0	523 3 US-09-095-855-114	Sequence 114, App
10	122	100.0	523 4 US-09-324-542-114	Sequence 114, App
11	122	100.0	523 4 US-09-205-426-114	Sequence 114, App
12	122	100.0	540 2 US-08-368-834-20	Sequence 20, App
13	122	100.0	540 4 US-08-461-722-3	Sequence 3, App
14	122	100.0	540 4 US-08-461-722-4	Sequence 4, App
15	122	100.0	540 4 US-08-336-251-3	Sequence 3, App
16	122	100.0	540 4 US-08-336-251-4	Sequence 3, App
17	122	100.0	540 4 US-09-468-041-3	Sequence 4, App
18	122	100.0	540 4 US-09-468-041-4	Sequence 4, App
19	122	100.0	540 4 US-09-613-303-4	Sequence 4, App
20	122	100.0	540 5 PCT-US94-06362-3	Sequence 3, App
21	122	100.0	540 5 PCT-US94-06362-4	Sequence 3, App
22	122	100.0	541 2 US-08-467-822-34	Sequence 34, App
23	122	100.0	541 2 US-08-447-154-19	Sequence 19, App
24	122	100.0	541 2 US-08-997-080-160	Sequence 160, App
25	122	100.0	541 2 US-08-997-362-160	Sequence 160, App
26	122	100.0	541 3 US-09-095-855-160	Sequence 160, App
27	122	100.0	541 3 US-08-432-697-34	Sequence 34, App

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28	122	100.0	541 3 US-08-466-248-34	Sequence 34, App
29	122	100.0	541 4 US-09-324-542-160	Sequence 160, App
30	122	100.0	541 4 US-09-205-426-160	Sequence 160, App
31	122	100.0	639 4 US-09-613-303-17	Sequence 29, App
32	122	100.0	648 4 US-09-613-303-29	Sequence 21, App
33	122	100.0	948 4 US-09-613-303-21	Sequence 6684, App
34	99	81.1	349 4 US-09-107-532A-6684	Sequence 2, App
35	98	80.3	547 4 US-08-461-722-2	Sequence 2, App
36	98	80.3	547 4 US-08-336-251-2	Sequence 2, App
37	98	80.3	547 4 US-09-468-041-2	Sequence 2, App
38	98	80.3	547 5 PCT-US94-06362-2	Sequence 2, App
39	98	80.3	548 2 US-08-467-822-31	Sequence 31, App
40	98	80.3	548 2 US-08-467-822-32	Sequence 32, App
41	98	80.3	548 3 US-09-472-971-3	Sequence 3, App
42	98	80.3	548 3 US-08-432-697-31	Sequence 31, App
43	98	80.3	548 3 US-08-432-697-32	Sequence 32, App
44	98	80.3	548 3 US-08-466-248-31	Sequence 31, App
45	98	80.3	548 3 US-08-466-248-32	Sequence 32, App

RESULT 1  
US-08-997-080-117  
Sequence 117, Application US/08997080  
Patent No. 5968524  
GENERAL INFORMATION:  
APPLICANT: WATSON, JAMES D.  
APPLICANT: TAN, PAUL L.J.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
NUMBER OF SEQUENCES: 194  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,080  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleath, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-997-080-117  
Query Match 100.0%; Score 122; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGRNVLEKKMGAPITINDG 22

DB 31 GPKGRNVLEKMGAPITINDG 52

## RESULT 2

US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiwama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match 100.0%; Score 122; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKMGAPITINDG 22

DB 31 GPKGRNVLEKMGAPITINDG 52

RESULT 3

US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match 100.0%; Score 122; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKMGAPITINDG 22

DB 31 GPKGRNVLEKMGAPITINDG 52

RESULT 4

US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul U.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 117

LENGTH: 215

TYPE: PRT

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 10.0741 Seconds  
(without alignments)  
152,738 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: \*  
2: p1r1: \*  
3: p1r2: \*  
4: p1r3: \*  
5: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	90	100.0	540	2	A26950
2	90	100.0	540	2	A43509
3	90	100.0	540	2	C41325
4	90	100.0	541	2	S40245
5	90	100.0	541	2	T44725
6	90	100.0	588	2	A25902
7	81	90.0	543	2	S70013
8	80	88.9	528	2	S73270
9	80	88.9	538	2	H72367
10	80	88.9	541	2	T06829
11	80	88.9	544	1	BVYCGI
12	80	88.9	544	1	AG2263
13	79	87.8	577	2	S20876
14	78	86.7	524	2	F84742
15	77	85.6	538	2	J01195
16	77	85.6	539	2	B49855
17	77	85.6	541	2	B44425
18	77	85.6	542	2	AC1704
19	77	85.6	542	2	AD1333
20	77	85.6	543	2	B41872
21	77	85.6	543	2	F97232
22	77	85.6	544	2	UC5130
23	77	85.6	544	2	B41884
24	77	85.6	544	2	JC6063
25	77	85.6	544	2	B83720
26	76	84.4	599	2	T07733
27	75	83.3	540	2	B41325
28	75	83.3	541	2	T35591
29	75	83.3	546	2	S34938

30	75	83.3	546	2	B47073	chaperonin GroEL -
31	74	82.2	534	2	S26877	groEL protein - re
32	74	82.2	541	2	S68249	chaperonin groEL h
33	74	82.2	552	2	S74322	chaperonin groEL-2
34	74	82.2	560	2	AB2043	chaperonin GroEL f
35	73	81.1	174	2	T07735	probable chaperoni
36	73	81.1	539	2	S22342	chaperonin HSP60 -
37	73	81.1	542	2	UN0661	heat shock protein
38	73	81.1	542	2	S32106	groEL protein - Ia
39	73	81.1	542	2	B86674	60 KD chaperonin f
40	73	81.1	546	2	I40342	heat shock protein
41	73	81.1	546	2	S22347	groEL - Brucella a
42	73	81.1	546	2	AG3640	60K chaperonin gro
43	73	81.1	547	2	B87334	chaperonin, 60 kDa
44	73	81.1	550	2	A41468	60K heat shock pro
45	73	81.1	588	2	PM0007	chaperonin 62.5K b

#### ALIGNMENTS

##### RESULT 1

A26950

groEL2 protein - Mycobacterium tuberculosis (strain H37RV)

N/Alternate names: 65K antigen

C/Species: Mycobacterium tuberculosis

C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 20-Jun-2000

C/Accession: A26950, A70830

R/Shimnick, T.M.

J. Bacteriol. 169, 1080-1088, 1987

A/Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.

A/Reference number: A26950; MUID:87137260; PMID:3029018

A/Accession: A26950

A/Molecule type: DNA

A/Residues: 1-540 <SH1>

A/Cross-references: GB:M15467; NID:G149999; PIDN:AA88232.1; PID:G150000

R/Comor, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.;

Rajandream, M.A.; Rogers, J.; Devlin, K.; Feltham, T.; Gentile, S.; Hamlin, N.; Holroyd, S.

Nature 393, 537-544, 1998

A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: A70830

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-540 <COL>

A/Cross-references: GB:AL021932; GB:AL123456; NID:G3261527; PIDN:CA17397.1; PID:G29095

A/Experimental source: strain H37RV

C/Genetics:

A/Gene: groEL2; RV0440

C/Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKMGAP 16  
Db 31 GPKGRNVLEKKMGAP 46

##### RESULT 2

A43509

65K antigen mba - Mycobacterium bovis

C/Species: Mycobacterium bovis

C/Date: 28-Oct-1992 #sequence\_revision 28-Oct-1992 #text\_change 26-Aug-1999

C/Accession: A43509

R/Thole, J.E.R.; Keulen, W.J.; Kolik, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema,

Infect. Immun. 55, 1466-1475, 1987

A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton

A/Reference number: A43509; MUID:87193155; PMID:3553003

A/Accession: A43509

A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-540 <THO>  
 A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934  
 C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 31 GPKGRNVLEKKWGAP 46

## RESULT 3

C41325  
 heat shock protein 56 - Streptomyces albus  
 N/Alternate names: heat shock protein groEL homolog 2  
 C/Species: Streptomyces albus  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 26-Aug-1999  
 C/Accession: C41325  
 R/Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.  
 J. Bacteriol. 173, 7382-7386, 1991  
 A>Title: Characterization of the groEL-like genes in Streptomyces albus.  
 A/Reference number: A41325; MUID:92041639; PMID:1682304  
 A/Accession: C41325  
 A:Molecule type: DNA  
 A:Residues: 1-540 <MA2>  
 A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294  
 C/Genetics:  
 A:Gene: groEL2  
 C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 31 GPKGRNVLEKKWGAP 46

## RESULT 4

S40245  
 heat shock protein 65 - Mycobacterium paratuberculosis  
 C/Species: Mycobacterium paratuberculosis  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
 C/Accession: S40245  
 R/Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.  
 submitted to the EMBL Data Library, August 1993  
 A/Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.  
 A/Reference number: S40245  
 A/Accession: S40245  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-541 <COL>  
 A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181  
 C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 31 GPKGRNVLEKKWGAP 46

## RESULT 5

T44725  
 chaperonin 60K [imported] - Mycobacterium leprae  
 N/Alternate names: heat shock protein GroEL-2

C/Species: Mycobacterium leprae  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
 C/Accession: T44725  
 R/James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, January 1998  
 A/Reference number: Z22831  
 A/Accession: T44725  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-541 <JAM>  
 A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1  
 A/Experimental source: cosmid B1450  
 C/Genetics:  
 A:Gene: groEL-2  
 C:Superfamily: chaperonin groEL  
 C/Keywords: molecular chaperone

Query Match 100.0%; Score 90; DB 2; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 31 GPKGRNVLEKKWGAP 46

## RESULT 6

A25902  
 65K antigen - Mycobacterium leprae  
 C/Species: Mycobacterium leprae  
 C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997  
 C/Accession: A25902  
 R/Mehra, V.; Sweetser, D.; Young, R.A.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986  
 A>Title: Efficient mapping of protein antigenic determinants.  
 A/Reference number: A25902; MUID:86313701; PMID:2428046  
 A:Molecule type: DNA  
 A:Residues: 1-588 <MEH>  
 C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 588;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 78 GPKGRNVLEKKWGAP 93

## RESULT 7

S70013  
 chaperonin-like protein groEL2 - Synechococcus sp.  
 C/Species: Synechococcus sp.  
 C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 20-Jun-2000  
 C/Accession: S70013; S70022  
 R/Purki, M.; Tanaka, N.; Hiya, T.; Nakamoto, H.  
 Biochim. Biophys. Acta 1294, 106-110, 1996  
 A>Title: Cloning, characterization and functional analysis of groEL-like gene from the  
 A/Reference number: S70013; MUID:96248387; PMID:8645726  
 A/Accession: S70013  
 A:Molecule type: DNA  
 A:Residues: 1-543 <PUR>  
 A:Cross-references: GB:D86184; EMBL:D17354; NID:g1408522; PIDN:BA13082.1; PID:g1228065  
 A/Note: the source is designated as Synechococcus vulcanus  
 A:Molecule type: protein  
 A:Residues: 2-11 <PUR>  
 A/Note: the source is designated as Synechococcus vulcanus  
 C/Genetics:  
 A:Gene: groEL2  
 C:Superfamily: chaperonin groEL  
 C/Keywords: heat shock



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 6.81482 Seconds  
(without alignments)  
110.411 Million cell updates/sec

Title: US-09-847-637B-2  
90

Perfect score: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	476	1	CH62_STRL1
2	90	100.0	539	1	CH60_TSUTY
3	90	100.0	539	1	CH62_MYCTU
4	90	100.0	539	1	CH62_STRL1
5	90	100.0	540	1	CH60_MYCPA
6	90	100.0	540	1	CH60_TSUPA
7	90	100.0	540	1	CH62_MYCLE
8	90	100.0	541	1	CH60_COREQ
9	90	100.0	541	1	CH60_NOCRA
10	90	100.0	541	1	CH62_STRCO
11	90	100.0	542	1	CH60_NOCAS
12	87	96.7	540	1	CH60_TROWT
13	85	94.4	544	1	CH60_PROAC
14	84	93.3	547	1	CH62_COREP
15	84	93.3	548	1	CH62_COREL
16	81	90.0	543	1	CH60_ANASL
17	81	90.0	543	1	CH62_SYNEL
18	80	88.9	300	1	CH60_SYNP6
19	80	88.9	528	1	CH60_PORPU
20	80	88.9	538	1	CH60_THENA
21	80	88.9	538	1	CH60_THENA
22	80	88.9	541	1	CH60_TYAPA
23	80	88.9	544	1	CH60_SYNP7
24	80	88.9	544	1	CH61_ANASP
25	80	88.9	544	1	CH61_SYNVU
26	80	88.9	545	1	CH60_SYNEL
27	79	87.8	543	1	CH60_BACFO
28	79	87.8	577	1	CH60_ARATH
29	78	86.7	529	1	CH60_GUITH
30	77	85.6	538	1	CH60_BACP3
31	77	85.6	538	1	CH60_BACST
32	77	85.6	539	1	CH60_BACST
33	77	85.6	540	1	CH60_RHOMR

34	77	85.6	540	1	CH61_SYNV3	O05972 synechocyst
35	77	85.6	542	1	CH60_LISIN	Q925V0 listeria in
36	77	85.6	542	1	CH60_LISMO	Q9A566 listeria mo
37	77	85.6	543	1	CH60_BACSV	P28598 bacillus su
38	77	85.6	543	1	CH60_BRECH	O8R000 brevbacillu
39	77	85.6	543	1	CH60_CLOAB	P30717 clostridium
40	77	85.6	544	1	CH60_BACHD	O50305 bacillus ha
41	76	84.4	530	1	CH60_CYACA	Q9L121 cyanidulium c
42	76	84.4	543	1	CH60_IACJO	Q9KJ23 lactobacillu
43	75	83.3	539	1	CH61_STRL1	O00767 streptomyc
44	75	83.3	540	1	CH61_STRCO	P40171 streptomyc
45	75	83.3	546	1	CH60_CHRY1	P31293 chromatiu

## ALIGNMENTS

RESULT 1  
CH62\_STRL1 STANDARD; PRT; 476 AA.  
ID CH62\_STRL1  
AC O33658;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-SEP-2003 (Rel. 41, Last annotation update)  
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).  
GN GROEL2 OR GROEL2.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=TK21;  
RX MEDLINE=98048481; PubMed=9387235;  
RA de Leon P, Marco S, Telegas C, Marina A, Carrascosa J.L.,  
RT Mellado R.P.,  
RT "Streptomyces lividans groEL1 and groEL2 genes";  
RL Microbiology 143:3563-3571(1997).  
CC -1- FUNCTION: Prevents misfolding and promotes the refolding and  
proper assembly of unfolded polypeptides generated under stress  
conditions (By similarity).  
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of  
7 subunits (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.  
CC  
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CC  
DR EMBL; X95971; CA65226.1; -.  
DR HSSP; P06139; IGRL.  
DR HAMAP; MF\_00600; atypical; 1.  
DR InterPro; IPR001844; Chaperon Cpn60.  
DR InterPro; IPR002423; Cpn60/TCF-1.  
DR Pfam; PF00118; Cpn60\_TCF1; 1.  
DR PRINTS; PR00298; CHAPERONIN60.  
DR PRINTS; PR00304; TCOMPLEXTCF1.  
DR PROSITE; PS00296; CHAPERONINS\_CPN60; 1.  
KW Chaperone; ATP-binding; Multigene family.  
FT INT MET 0  
FT SEQUENCE 476 AA; 50529 MW; 760F81793F4F5D4D CRC64;  
Query Match 100.0%; Score 90; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGRNVLEKKMGAP 16  
|||||

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Db          30  GPKGRNVLEKKMGAP 45

RESULT 2
CH60_TSUTY
ID   CH60_TSUTY          STANDARD;          PRT;          539 AA.
DC   P97086;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein
    60). OR GROEL OR HSP60.
OS   Tsukamurella tyrosinosolvens.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacteriaceae; Tsukamurellaceae; Tsukamurella.
OX   NCBI_TaxID=57704;
[1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IMMIB D-1411;
RA   Zimmermann O., Pinkenburg O., Koechel H.G.;
RT   "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
    protein 60."
RL   Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
CC   -1- FUNCTION: Prevents misfolding and promotes the refolding and
    proper assembly of unfolded polypeptides generated under stress
    conditions (by similarity).
CC   -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
    7 subunits (by similarity).
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC   -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
-----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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    or send an email to license@isb-sib.ch).
-----
CC   EMBL: U90204; ABA849990.1; -.
DR   HSP60, P06139, IGRIL.
DR   HAMMP, MF_006000; -.
DR   InterPro: IPR001844; Chaperin_Cpn60.
DR   InterPro: IPR002423; Cpn60/TCP-1.
DR   Pfam: PF00118; Cpn60_TCP1, 1.
DR   PRINTS: PR00298; CHAPERONIN60.
DR   PRINTS: PR00304; TCOMPLEXTCP1.
DR   PROSITE: PS00296; CHAPERONINS_CPN60, 1.
SQ   Chaperone; ATP-binding.
SQ   SEQUENCE 539 AA; 56137 MW; 6355314830C9B662 CRC64;

Query Match          100.0%; Score 90; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          1  GPKGRNVLEKKMGAP 16
           |||||
Db          31  GPKGRNVLEKKMGAP 46

RESULT 3
CH62_MYCTU
ID   CH62_MYCTU          STANDARD;          PRT;          539 AA.
AC   P06806; Q48920; Q48931;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (Antigen A).
DE   antiGen (Heat shock protein 60) (Cell wall protein 2) (65 kDa
    antiGen) (Heat shock protein 60) (Cell wall protein 2) (Antigen A).
GN   GRO12 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.
OS   Mycobacterium tuberculosis, and

```

CC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OK NCBI\_TaxID=1773, 1765;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=Erkdmann;  
 RX MEDLINE=87137260; PubMed=5029018;  
 RA Shinnick T.M.;  
 RL "The 65-kilodalton antigen of Mycobacterium tuberculosis.",  
 RN J. Bacteriol. 169:1080-1088 (1987).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=H37Rv;  
 RX MEDLINE=96259587; PubMed=5634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gass S., Barry C.E. III, Tekala F.,  
 RA Badoock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Kerekh A., Hamlin N., Holtroyd S.,  
 RA Hornsby T., Jagels K., Krogell A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Ruster S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultson J.E., Taylor K., Whitehead S., Barrall B.G.,  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.",  
 RL Nature 393:537-544 (1998).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gaitn M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayan L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bhal G.;  
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.",  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=M.bovis; STRAIN=BCG;  
 RX MEDLINE=87193155; PubMed=3535003;  
 RA Thole J.E.R., Kuilen W.J., Kolik A.H.J., Groothuis D.G., Berwald L.G.,  
 RA Tiesjema R.H., van Embden J.D.A.;  
 RT "Characterization, sequence determination, and immunogenicity of a  
 RT 64-kilodalton protein of Mycobacterium bovis BCG expressed in  
 RL Escherichia coli K-12.",  
 RN Infect. Immun. 55:1466-1475 (1987).  
 RN [5]  
 RN SEQUENCE OF 45-195 FROM N.A.  
 RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;  
 RX Roe C., Belak K.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN SEQUENCE OF 63-182 FROM N.A.  
 RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TWC 410, and TWC 1024;  
 RX MEDLINE=95150784; PubMed=7848059;  
 RA Kapur V., Li L.B., Hamrick M.R., Plikaytis B.B., Shinnick T.M.,  
 RA Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y.,  
 RA Claridge J.E., Kreiswirth B.N., Musher J.M.;  
 RT "Rapid Mycobacterium species associated with antitubercular resistance  
 RT identification of mutations associated with antitubercular resistance  
 RT in Mycobacterium tuberculosis by automated DNA sequencing.",  
 RL Arch. Pathol. Lab. Med. 119:131-138 (1995).  
 RN [7]  
 RN SEQUENCE OF 64-177 FROM N.A.  
 RC SPECIES=M.tuberculosis;  
 RX MEDLINE=95214306; PubMed=7699930;  
 RA Hidaka E., Ueno I., Kawakami Y., Furuwatari C., Furuhata K.,  
 RA Katayama T.;  
 RL "Detection and identification of mycobacteria by PCR-RFLP method.",  
 RL Rinho Bvori 43:155-161 (1995).  
 CC -I- FUNCTION: Prevents misfolding and promotes the refolding and  
 CC proper assembly of unfolded polypeptides generated under stress  
 CC conditions (By similarity).

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# OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 25.7778 Seconds  
(without alignments)  
160.171 Million cell updates/sec

Title: US-09-847-637B-2  
Perfect score: 90  
Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_nhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	59	2	Q9EMD1
2	90	100.0	61	2	Q9EUR7
3	90	100.0	539	2	P97086
4	90	100.0	540	2	Q9AFAS
5	90	100.0	541	2	Q93Q12
6	90	100.0	541	2	Q9AF66
7	90	100.0	541	2	Q9KGM1
8	90	100.0	542	2	Q9AFCS
9	90	100.0	548	2	Q8GARS
10	90	100.0	548	2	Q8GAR7
11	90	100.0	548	2	Q8G923
12	90	100.0	548	2	Q8G8X0
13	90	100.0	549	2	Q8GAR9
14	85	94.4	533	2	Q9PDS2
15	84	93.3	547	16	Q8CY22
16	84	93.3	548	16	Q8NM64

17	81	90.0	543	2	Q9AMJ8	Q9amj8 anabaena sp
18	80	88.9	545	16	Q8DMD4	Q8dmd4 synechococc
19	78	86.7	524	10	Q49314	Q49314 arabidopsis
20	78	86.7	585	10	Q8L7B5	Q8l7b5 arabidopsis
21	77	85.6	539	2	Q9EZV4	Q9ezv4 bacillus st
22	77	85.6	539	2	Q9RC20	Q9rc20 bacillus st
23	77	85.6	545	2	Q8GB95	Q8gb95 heliobacill
24	77	85.6	581	5	Q46219	Q46219 culicoides
25	76	84.4	598	5	Q9XYR7	Q9xyr7 onchocerca
26	76	84.4	599	10	P93570	P93570 solanum tub
27	75	83.3	546	2	Q31198	Q31198 leptospira
28	75	83.3	573	5	Q9USN2	Q9usn2 myzus persi
29	75	83.3	576	5	Q8WZB0	Q8wzb0 drosophila
30	75	83.3	576	5	Q8WZM9	Q8wzm9 trichinella
31	75	83.3	576	5	Q8IHD0	Q8ihd0 drosophila
32	75	83.3	580	5	Q96783	Q96783 plectus acu
33	75	83.3	582	5	Q9USL7	Q9usl7 paracentrot
34	74	82.2	543	2	Q8KZN2	Q8kzn2 thermus sp.
35	74	82.2	545	16	Q8CX13	Q8cx13 oceanobacil
36	73	81.1	174	10	P93571	P93571 solanum tub
37	73	81.1	531	2	Q8GBD0	Q8gbd0 enterococcu
38	73	81.1	531	2	Q8GBC6	Q8gbc6 enterococcu
39	73	81.1	531	2	Q8GBC4	Q8gbc4 enterococcu
40	73	81.1	531	2	Q8GBC2	Q8gbc2 enterococcu
41	73	81.1	531	2	Q8GBC0	Q8gbc0 enterococcu
42	73	81.1	532	2	Q8GBC8	Q8gbc8 enterococcu
43	73	81.1	532	2	Q8GBB8	Q8gbb8 enterococcu
44	73	81.1	532	16	Q8CWD0	Q8cwo0 vibrio vuln
45	73	81.1	537	2	Q9K171	Q9k171 parascardov

## ALIGNMENTS

RESULT 1	ID	Q9EMD1	PRELIMINARY:	PRT:	59 AA.
AC	Q9EMD1				
DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Heat-shock protein (Fragment).				
GN	GROEL2				
OS	Streptomyces coelicolor.				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Streptomycinae; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxId=1902;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=J802;				
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.,				
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces				
RT	antibiotic biosynthesis."				
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
RU					
DR	EMBL; AJ250536; CAC19351.1; -				
DR	HSSP; P06139; IACN.				
DR	InterPro; IPR002423; Cpn60/TCP-1.				
DR	Pfam; PF00118; cpn60 TCP1; 1.				
DR	PRINTS; PR00304; TCOMPLEXTCP1.				
KW	ATP-binding; Chaperone.				
FT	NON TER				
SQ	SEQUENCE 59 AA; 6407 MW; E7B24199B7DB68FA CRC64;				
Query Match					
Best Local Similarity	100.0%; Score 90; DB 2; Length 59;				
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GPKGRNVVLEKKMGAP 16				
DB	31 GPKGRNVVLEKKMGAP 46				
RESULT 2					

```

09EUR7
ID 09EUR7 PRELIMINARY; PRT; 61 AA.
AC 09EUR7;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Heat-shock protein (Fragment).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteriia; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; Cpn60 TCP1. 1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
KM ATP-binding; Chaperone.
FT NCN TER 61
SQ SEQUENCE 61 AA; 6645 MW; D200995P4199B7CA CRC64;

Query Match 100.0%; Score 90; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. NO. 8.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKGWGP 16
Db 31 GPKGRNVLEKKGWGP 46

RESULT 3
P97086 PRELIMINARY; PRT; 539 AA.
AC P97086;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella tyrosinosevens.
OC Bacteria; Actinobacteriia; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koeschel H.G.;
RT "Tsukamurella tyrosinosevens sp. nov. hsp60 gene for heat shock
RT protein 60.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RN EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; Cpn60 TCP1. 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KM ATP-binding; Chaperone.
FT NCN TER 540
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. NO. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKGWGP 16
Db 31 GPKGRNVLEKKGWGP 46

RESULT 5
093012 PRELIMINARY; PRT; 541 AA.
AC 093012;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteriia; Actinobacteriia; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 90; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. NO. 8.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKGWGP 16
Db 31 GPKGRNVLEKKGWGP 46

RESULT 4
09AFAS PRELIMINARY; PRT; 540 AA.
AC 09AFAS;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteriia; Actinobacteriia; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koeschel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RN EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; Cpn60 TCP1. 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KM ATP-binding; Chaperone.
FT NCN TER 540
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. NO. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKGWGP 16
Db 31 GPKGRNVLEKKGWGP 46

RESULT 5
093012 PRELIMINARY; PRT; 541 AA.
AC 093012;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteriia; Actinobacteriia; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 31.4074 Seconds  
(without alignments)  
80.861 Million cell updates/sec

Title: US-09-847-637B-2  
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_19Jun03.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	16	AA193329	Amino acid sequenc
2	90	100.0	16	AAU99964	Mycobacterium tube
3	90	100.0	22	AA193328	Amino acid sequenc
4	90	100.0	215	AAW60145	M. vaccae antigen
5	90	100.0	215	AA14892	Amino acid sequenc
6	90	100.0	215	ABW73498	M vaccae GroEL hom
7	90	100.0	295	AA191615	Amino acid sequenc
8	90	100.0	523	AAW60144	M. vaccae antigen
9	90	100.0	523	AA14891	Amino acid sequenc

10	90	100.0	523	ABW73497	M vaccae GroEL hom
11	90	100.0	539	AA193319	Amino acid sequenc
12	90	100.0	540	AA191351	Sequence of Mycoba
13	90	100.0	540	AA198160	Mycobacterium tube
14	90	100.0	540	AAW32100	Mycobacterium sp. h
15	90	100.0	540	AAW44702	Mycobacterium tube
16	90	100.0	540	AA193911	Amino acid sequenc
17	90	100.0	540	AA193332	Amino acid sequenc
18	90	100.0	540	AAE11755	Mycobacterium tube
19	90	100.0	540	AA198118	Mycobacterium tube
20	90	100.0	540	AA1931606	Amino acid sequenc
21	90	100.0	540	AAU76511	M. leprae 65kDa at
22	90	100.0	540	AAU76511	M. tuberculosis 65
23	90	100.0	540	AAU76193	Mycobacterium lepr
24	90	100.0	540	AAU76194	Mycobacterium tube
25	90	100.0	540	AAW50750	Mycobacterium tube
26	90	100.0	540	ABG74587	M. leprae 65kDa at
27	90	100.0	540	ABG74588	M. tuberculosis 65
28	90	100.0	541	AA198784	M. leprae GroEL g
29	90	100.0	541	AA194909	Amino acid sequenc
30	90	100.0	541	AA193910	Amino acid sequenc
31	90	100.0	541	AA193913	Amino acid sequenc
32	90	100.0	541	AA193913	Amino acid sequenc
33	90	100.0	544	AA193209	M vaccae GroEL hom
34	90	100.0	560	AA1980215	Mycobacteria sp. h
35	90	100.0	572	AA19804716	Sequence of Mycoba
36	90	100.0	573	AA19804715	Amino acid sequenc
37	90	100.0	573	AA19804715	Amino acid sequenc
38	90	100.0	573	AA19804715	M. leprae 65 kDa p
39	90	100.0	588	AA19804715	M. tuberculosis 65
40	90	100.0	638	AA19803790	M. leprae 65kD ant
41	90	100.0	639	AA19803790	Heat shock protein
42	90	100.0	639	AA19803790	Amino acid sequenc
43	90	100.0	648	AA19803790	Amino acid sequenc
44	90	100.0	690	ABG70777	BCG Hsp65/mutant H
45	90	100.0	709	ABG70776	BCG Hsp65/mutant H
			724	ABG70778	BCG Hsp65/mutant H

## ALIGNMENTS

RESULT 1	AA193329	standard; peptide; 16 AA.
ID	AA193329	
AC	AA193329	
DT	04-SEP-2000	(first entry)
DE	Amino acid sequence of an epitope of heat shock protein 60.	
XX	Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;	
XX	Inflammatory disorder; arthritis.	
OS	Mycobacterium tuberculosis.	
XX	MO200027870-A1.	
PD	18-MAY-2000.	
XX	04-NOV-1999;	99WO-IL00595.
XX	05-NOV-1998;	98US-0107213.
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.	
PI	Naparetek Y, Umaneky R, Kaeshi Y;	
XX	WPI; 2000-376486/32.	
DR	Peptide having a defined sequence is used in vaccines for conferring	
XX	immunity against autoimmune disease or inflammatory disorders,	
PT	especially arthritis -	

XX Claim 2; Page 7; 58pp; English.  
 PS  
 XX  
 CC The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 90; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 Db 1 GPKGRNVLEKKWGAP 16  
 RESULT 2  
 ID AAU99964 standard; Peptide; 16 AA.  
 AC AAU99964;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.  
 XX  
 KM Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 KM autoimmune disease; infectious disease; graft rejection; type 1 diabetes;  
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 KM arteriosclerosis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200248312-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 11-DEC-2001; 2001WO-1L01144.  
 XX  
 PR 11-DEC-2000; 2000IL-0140233.  
 XX  
 PA (PEPT-) PEPTOR LTD.  
 XX  
 PI Bias D, Avron A, Senderowitz H;  
 XX  
 DR WPI; 2002-557613/59.  
 XX  
 PT New backbone cyclised peptide analog of heat shock protein useful in  
 PT the treatment of e.g. autoimmune disease -  
 XX  
 PS Claim 5; Page 42; 50pp; English.  
 XX  
 CC The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type 1 diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 90; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
 Db 1 GPKGRNVLEKKWGAP 16  
 RESULT 3  
 ID AA93328 standard; peptide; 22 AA.  
 AC AA93328;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of an epitope of heat shock protein 60.  
 XX  
 KM Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KM inflammatory disorder; arthritis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200027870-A1.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PE 04-NOV-1999; 99WO-IL00595.  
 XX  
 PR 05-NOV-1998; 98US-0107213.  
 XX  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX  
 PI Naparstek Y, Ulanovsky R, Kasbi Y;  
 XX  
 DR WPI; 2000-376486/32.  
 XX  
 PT Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -  
 XX  
 PS Claim 1; Page 7; 58pp; English.  
 XX  
 CC The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX  
 SQ Sequence 22 AA;  
 Query Match 100.0%; Score 90; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGAP 16  
 Db 1 GPKGRNVLEKKWGAP 16  
 RESULT 4  
 ID AAW60145 standard; Protein; 215 AA.  
 AC AAW60145;  
 XX  
 DT 25-AUG-1998 (first entry)  
 XX  
 DE M. vaccae antigen GV-27A sequence.  
 XX  
 KM Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KM mycobacteria infection; vaccine; cancer.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:09:39 ; Search time 21.9259 Seconds  
(without alignments)  
145.229 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 5: /cgm2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
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- 14: /cgm2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 15: /cgm2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgm2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgm2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgm2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	90	100.0	22	10	US-09-847-637B-1
3	90	100.0	215	11	US-09-880-505-117
4	90	100.0	215	12	US-10-205-979-411
5	90	100.0	215	14	US-10-051-643-117
6	90	100.0	295	15	US-10-267-311-33
7	90	100.0	523	11	US-09-880-505-114
8	90	100.0	523	14	US-10-051-643-114
9	90	100.0	540	10	US-09-847-637B-6
10	90	100.0	540	10	US-09-712-363-169
11	90	100.0	540	15	US-10-267-311-4
12	90	100.0	540	15	US-10-046-649-3
13	90	100.0	540	15	US-10-046-649-4
14	90	100.0	541	11	US-09-880-505-160
15	90	100.0	541	12	US-10-205-979-40

16	90	100.0	541	14	US-10-051-643-160	Sequence 160, App
17	90	100.0	541	15	US-10-156-761-11465	Sequence 11465, A
18	90	100.0	576	12	US-10-369-493-8322	Sequence 8322, Ap
19	90	100.0	639	15	US-10-267-311-17	Sequence 17, Appl
20	90	100.0	648	15	US-10-267-311-29	Sequence 29, Appl
21	90	100.0	690	14	US-10-068-059-10	Sequence 10, Appl
22	90	100.0	709	14	US-10-068-059-8	Sequence 8, Appl
23	90	100.0	724	14	US-10-068-059-12	Sequence 12, Appl
24	90	100.0	746	14	US-10-068-059-6	Sequence 6, Appl
25	90	100.0	948	15	US-10-267-311-21	Sequence 21, Appl
26	84	93.3	548	10	US-09-738-626-6486	Sequence 6486, Ap
27	82	91.1	537	12	US-10-369-493-10014	Sequence 10014, A
28	80	88.9	548	12	US-10-369-493-2950	Sequence 2950, Ap
29	80	88.9	544	12	US-10-369-493-20276	Sequence 20276, A
30	80	88.9	544	12	US-10-369-493-20873	Sequence 20873, A
31	79	87.8	545	12	US-10-369-493-19756	Sequence 19756, A
32	77	85.6	544	12	US-10-369-493-17132	Sequence 17132, A
33	77	85.6	544	12	US-10-369-493-23094	Sequence 23094, A
34	77	85.6	551	12	US-10-369-493-20184	Sequence 20184, A
35	75	83.3	521	12	US-10-369-493-9597	Sequence 9597, Ap
36	75	83.3	540	12	US-10-369-493-15838	Sequence 15838, A
37	75	83.3	542	15	US-10-156-761-12526	Sequence 12526, A
38	75	83.3	544	12	US-10-369-493-15468	Sequence 15468, A
39	75	83.3	544	12	US-10-369-493-16217	Sequence 16217, A
40	74	82.2	551	12	US-10-369-493-18994	Sequence 18994, A
41	74	82.2	552	12	US-10-369-493-2799	Sequence 2799, Ap
42	73	81.1	547	15	US-10-369-493-10235	Sequence 10235, A
43	72	80.0	547	15	US-10-046-649-2	Sequence 2, Appl
44	72	80.0	548	11	US-09-415-849-1	Sequence 1, Appl
45	72	80.0	548	11	US-09-276-455-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-09-847-637B-2  
; Sequence 2, Application US/09847637B  
; Patent No. US20020150586A1  
; GENERAL INFORMATION:  
; APPLICANT: Naparstek, Yaakov  
; APPLICANT: Umanetsky, Rina  
; APPLICANT: Kashi, Yechezkel  
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF  
; FILE REFERENCE: 13125-002001  
; CURRENT APPLICATION NUMBER: US/09/847,637B  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: PCT/IL99/00595  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,213  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-847-637B-2  
Query Match 100.0%; Score 90; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 GPKGRNVVLEKKMGAP 16  
DB 1 GPKGRNVVLEKKMGAP 16  
RESULT 2  
US-09-847-637B-1  
; Sequence 1, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Napaterek, Yaakov
; APPLICANT: Napaterek, Rina
; APPLICANT: Ulanovsky, Rina
; APPLICANT: Kashi, Yecheskel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-847-637B-1

Query Match      100.0%; Score 90; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      1 GPKGRNVVLEKKWGAP 16

RESULT 3
US-09-880-505-117
; Sequence 117, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-09-880-505-117

Query Match      100.0%; Score 90; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 4
US-10-205-979-41
; Sequence 41, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.

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; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-10-205-979-41

Query Match      100.0%; Score 90; DB 12; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 5
US-10-051-643-117
; Sequence 117, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-10-051-643-117

Query Match      100.0%; Score 90; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 6
US-10-267-311-33
; Sequence 33, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10

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GenCore version 5.1.6  
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OM protein - protein search, using sw model1

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(Without alignments)  
60.126 Million cell updates/sec

Title: US-09-847-637B-2

Sequence: 1 GPKGRNVLEKKWGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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6	90	100.0	295 4	US-09-613-303-33 Sequence 33, App1
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23	90	100.0	541 2	US-08-997-080-160 Sequence 160, App
24	90	100.0	541 2	US-08-997-362-160 Sequence 160, App
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27	90	100.0	541 3	US-08-432-697-34 Sequence 34, App1

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30	90	100.0	541 4	US-09-205-426-160 Sequence 160, App
31	90	100.0	639 4	US-09-613-303-17 Sequence 29, App1
32	90	100.0	648 4	US-09-613-303-29 Sequence 29, App1
33	90	100.0	948 4	US-09-613-303-21 Sequence 21, App1
34	73	81.1	349 4	US-09-107-532A-6684 Sequence 6684, App
35	73	81.1	548 2	US-08-467-822-31 Sequence 31, App1
36	73	81.1	548 3	US-08-432-697-31 Sequence 31, App1
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39	72	80.0	547 4	US-08-336-251-2 Sequence 2, App11
40	72	80.0	547 4	US-09-468-041-2 Sequence 2, App11
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## ALIGNMENTS

RESULT 1  
US-08-997-080-117  
Sequence 117, Application US/08997080  
Patent No. 5968524  
GENERAL INFORMATION:  
APPLICANT: WATSON, JAMES D.  
APPLICANT: TAN, PAUL L.J.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
CORRESPONDENCE ADDRESSES: 194  
ADDRESS: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSSO for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,080  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleeth, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-997-080-117

Query Match 100.0%; Score 90; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6, 1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGRNVLEKKWGAP 16

Db 31 GPKGRNVLEKKMGAP 46

# RESULT 2

US-08-997-362-117  
Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyma, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match 100.0%; Score 90; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 6,1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 GPKGRNVLEKKMGAP 46

1 GPKGRNVLEKKMGAP 16

US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Compounds and Methods for Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match 100.0%; Score 90; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 6,1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 GPKGRNVLEKKMGAP 46

1 GPKGRNVLEKKMGAP 16

US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 117

LENGTH: 215

TYPE: PRT

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 10.0741 Seconds  
(without alignments)  
152.738 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKRWGAPITINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	87	100.0	540 2 A26950	groEL2 protein - M
2	87	100.0	540 2 A43509	65K antigen mbaA -
3	87	100.0	540 2 A41325	heat shock protein
4	87	100.0	541 2 S40245	heat shock protein
5	87	100.0	541 2 T44725	chaperonin 60K (im
6	87	100.0	588 2 A25902	65K antigen - Myco
7	77	88.5	538 2 H72367	groEL protein - Th
8	72	82.8	540 2 S37566	groEL protein - S
9	72	82.8	540 2 B41325	heat shock protein
10	72	82.8	541 2 T35591	chaperonin cpn60 -
11	71	81.6	541 2 S72614	chaperonin 60 - Th
12	68	78.2	538 2 UQ1195	heat shock protein
13	68	78.2	539 2 B49855	heat shock protein
14	68	78.2	542 2 A21333	class I heat-shock
15	68	78.2	542 2 AD1333	class I heat-shock
16	68	78.2	543 2 B41872	heat shock protein
17	68	78.2	543 2 F97232	chaperonin GroEL,
18	68	78.2	544 2 UC5130	heat shock protein
19	68	78.2	544 2 B41884	58K heat shock pro
20	68	78.2	544 2 JC6063	chaperonin groEL -
21	68	78.2	544 2 BB3720	class I heat-shock
22	67	77.0	543 2 S70013	chaperonin-like pr
23	66	75.9	528 2 S73270	chaperonin, 60K -
24	66	75.9	541 2 T06829	chaperonin GroEL
25	66	75.9	544 2 AG2263	chaperonin GroEL
26	66	75.9	546 2 S34938	heat shock protein
27	66	75.9	548 2 G75499	groEL protein - De
28	66	75.9	550 2 A41468	60K heat shock pro
29	65	74.7	541 2 S68249	chaperonin groEL h

30	65	74.7	544 1 BVCGL	chaperonin groEL -
31	65	74.7	546 2 B47073	chaperonin groEL -
32	64	73.6	535 2 JC7858	GroEL protein - Te
33	64	73.6	539 2 S22342	chaperonin HSP60 -
34	64	73.6	542 2 UN0651	heat shock protein
35	64	73.6	542 2 S32106	groEL protein - La
36	64	73.6	542 2 B86574	60 KD chaperonin
37	63	72.4	540 2 G95222	chaperonin, 60 kDa
38	63	72.4	540 2 H98086	chaperonin GroEL
39	63	72.4	544 2 B82048	chaperonin, 60 kDa
40	63	72.4	547 2 JC4519	heat-shock protein
41	63	72.4	547 2 B43606	heat shock protein
42	63	72.4	547 2 B89203	heat shock protein
43	63	72.4	547 2 B83098	groEL protein PA43
44	63	72.4	548 1 BVCGL	chaperonin groEL
45	63	72.4	548 2 D91269	chaperonin GroEL

#### ALIGNMENTS

RESULT 1  
A26950  
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)  
N/Alternate names: 65K antigen  
C/Species: Mycobacterium tuberculosis  
C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 20-Jun-2000  
C/Accession: A26950; A70830  
R/Shimnick, T.M.  
J. Bacteriol. 169, 1080-1088, 1987  
A/Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.  
A/Reference number: A26950; MUID:87137260; PMID:3029018  
A/Accession: A26950  
A/Molecule type: DNA  
A/Residues: 1-540 <SH1>  
A/Cross-references: GB:M5467; NID:g149999; PIDN:AA88232.1; PID:g150000  
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A/Reference number: A70500; MUID:96295987; PMID:9634230  
A/Accession: A70830  
A/Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-540 <COL>  
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CA17397.1; PID:g29095  
C/Genetic: A70500  
C/Experimental source: strain H37RV  
A/Accession: A70500  
C/Suprafamily: chaperonin groEL

Query Match 100.0% Score 87; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VVLEKRWGAPITINDG 16  
DB 37 VVLEKRWGAPITINDG 52

RESULT 2  
A43509  
65K antigen mbaA - Mycobacterium bovis  
C/Species: Mycobacterium bovis  
C/Date: 28-Oct-1992 #sequence\_revision 28-Oct-1992 #text\_change 26-Aug-1999  
C/Accession: A43509  
R/Thole, J.B.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema, I.  
Infect. Immun. 55, 1466-1475, 1987  
A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton  
A/Reference number: A43509; MUID:87193155; PMID:3553003  
A/Accession: A43509

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <THO>  
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKKGAPTTINDG 16  
DB 37 VVLEKKKGAPTTINDG 52

## RESULT 3

C41325  
heat shock protein 56 - Streptomyces albus  
N:Alternate names: heat shock protein groEL homolog 2  
C:Species: Streptomyces albus  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 26-Aug-1999

C:Accession: C41325  
R:Matzdiel, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.  
J. Bacteriol. 173, 7382-7386, 1991  
A:Title: Characterization of the groEL-like genes in Streptomyces albus.  
A:Reference number: A41325; MUID:92041639; PMID:1682304  
A:Accession: C41325  
A:Molecule type: DNA  
A:Residues: 1-540 <MAZ>  
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294  
C:Genetics:

A:Gene: groEL2  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKKGAPTTINDG 16  
DB 37 VVLEKKKGAPTTINDG 52

## RESULT 4

S40245  
heat shock protein 65 - Mycobacterium paratuberculosis  
C:Species: Mycobacterium paratuberculosis  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
C:Accession: S40245  
R:Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdos, R.  
submitted to the EMBL Data Library, August 1993  
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65MD.  
A:Reference number: S40245  
A:Accession: S40245  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <COL>  
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKKGAPTTINDG 16  
DB 37 VVLEKKKGAPTTINDG 52

## RESULT 5

T44725  
Chaperonin 60K [imported] - Mycobacterium leprae  
N:Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T44725  
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z22831  
A:Accession: T44725  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-541 <JAM>  
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1  
A:Experimental source: cosmid B1450  
C:Genetics:

A:Gene: groEL-2  
C:Superfamily: chaperonin groEL  
C:Keywords: molecular chaperone

Query Match 100.0%; Score 87; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKKGAPTTINDG 16  
DB 37 VVLEKKKGAPTTINDG 52

## RESULT 6

A25902  
65K antigen - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C>Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997  
C:Accession: A25902  
R:Mehta, V.; Sweetser, D.; Young, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986  
A:Title: Efficient mapping of protein antigenic determinants.  
A:Reference number: A25902; MUID:86313701; PMID:2428046  
A:Accession: A25902  
A:Molecule type: DNA  
A:Residues: 1-588 <MEH>  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKKGAPTTINDG 16  
DB 84 VVLEKKKGAPTTINDG 99

## RESULT 7

H72367  
groEL protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: H72367  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: H72367  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-538 <ARN>  
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:ADJ35591.1; PID:g498101  
A:Experimental source: strain MSB8  
C:Genetics:

A:Gene: TM0506  
C:Superfamily: chaperonin groEL

Query Match 88.5%; Score 77; DB 2; Length 538;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 6.81482 Seconds  
(without alignments)  
110.411 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VLEKKMGAPITNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	87	100.0	476 1 CH62_STRLI	033658 streptomyc
2	87	100.0	539 1 CH60_TSTUT	P97086 taukumurell
3	87	100.0	539 1 CH62_MYCTU	P67806 mycobacteri
4	87	100.0	539 1 CH62_STRAL	Q00768 streptomyc
5	87	100.0	540 1 CH60_MYCPA	P42384 mycobacteri
6	87	100.0	540 1 CH62_TSTUPA	Q9af5 taukumurell
7	87	100.0	540 1 CH62_MYCTE	P99279 mycobacteri
8	87	100.0	541 1 CH60_COREQ	Q93q42 corynebacte
9	87	100.0	541 1 CH60_NOCFA	Q9af6 nocardia fa
10	87	100.0	541 1 CH62_STRCO	Q9kx5 streptomyc
11	87	100.0	542 1 CH60_NOCAS	Q9af5 nocardia as
12	82	94.3	540 1 CH60_TROWT	Q9kic0 tropheryma
13	82	94.3	544 1 CH60_PROAC	Q9k24 propionibac
14	81	93.1	547 1 CH62_COREF	Q8cy22 corynebacte
15	81	93.1	548 1 CH62_CORGL	Q8m64 corynebacte
16	77	88.5	538 1 CH60_THEMA	Q9wyx6 thermotoga
17	77	88.5	538 1 CH60_THEMA	Q9ey1 thermotoga
18	72	82.8	539 1 CH61_STRAL	P40111 streptomyc
19	72	82.8	540 1 CH61_STRCO	P40111 streptomyc
20	71	81.6	540 1 CH60_THBR	Q60024 thermoaer
21	70	80.5	537 1 CH60_PARDN	Q9k171 paracardov
22	70	80.5	540 1 CH60_THRTN	Q8r5c7 thermoaer
23	70	80.5	541 1 CH60_GARVA	Q9k157 garderella
24	69	79.3	537 1 CH60_BIFPA	Q93m78 bifidobacte
25	69	79.3	538 1 CH60_SCALO	Q9ey76 scaritovya
26	69	79.3	541 1 CH60_BIFLO	Q8g879 bifidobacte
27	69	79.3	582 1 CH60_BIFLO	Q9eyu4 bifidobacte
28	68	78.2	538 1 CH60_BACP3	P26209 bacillus ps
29	68	78.2	539 1 CH60_BACP3	Q07201 bacillus ac
30	68	78.2	539 1 CH60_BACTR	Q8v94 bacillus th
31	68	78.2	542 1 CH60_LISIN	Q929v0 listeria in
32	68	78.2	542 1 CH60_LISMO	Q9age6 listeria mo
33	68	78.2	542 1 CH60_THETH	P45746 thermus the

34	68	78.2	543 1 CH60_BACSU	P28598 bacillus eu
35	68	78.2	543 1 CH60_BRECH	Q8nu00 brevbacilli
36	68	78.2	543 1 CH60_CIOAB	P30717 clostridium
37	68	78.2	544 1 CH60_BACHD	Q05035 bacillus ha
38	67	77.0	539 1 CH60_FUSNN	Q8r5x7 fusobacteri
39	67	77.0	539 1 CH60_FUSNP	Q8g100 fusobacteri
40	67	77.0	540 1 CH60_RHOMR	Q9xca9 rhodochernu
41	67	77.0	540 1 CH61_STRLI	Q33659 streptomyc
42	67	77.0	543 1 CH60_ANASL	Q9amj8 anabaena sp
43	67	77.0	543 1 CH60_LACJO	Q9k123 lactobacilli
44	67	77.0	543 1 CH62_SYNEI	Q57002 synecococc
45	66	75.9	528 1 CH60_PORPU	P51349 porphyra pu

## ALIGNMENTS

## RESULT 1

CH62\_STRLI STANDARD; PRT; 476 AA.  
ID CH62\_STRLI  
AC O33658;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 60 kDa chaparonin 2 (Protein Cpn60 2) (GroEL2 protein).  
GN GROEL2 OR GROEL2.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxId=1916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TX21;  
RX MEDLINE=98048481; PubMed=9387235;  
RA de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.,  
RA Melledo R.P.,  
RT "Streptomyces lividans groEL1 and groEL2 genes";  
RL Microbiology 143:3563-3571 (1997).  
CC -1- FUNCTION: Prevents misfolding and promotes the refolding and  
proper assembly of unfolded polypeptides generated under stress  
conditions (By similarity).  
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of  
7 subunits (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the chaparonin (HSP60) family.

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the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: X95971; CA65226.1; -;  
DR HAMAP: MF06139; IGRL.  
DR HAMAP: MF06600; atypical.1.  
DR InterPro: IPR001844; Chaparnin Cpn60.  
DR InterPro: IPR002423; Cpn60/TCF-1.  
DR Pfam: PF00118; Cpn60\_TCF1.1.  
DR PRINTS: PR00298; CHAPERONIN60.  
DR PRINTS: PR00304; TCOMPLEXTCPI.  
DR PROSITE: PS00296; CHAPERONINS\_CPN60\_1.  
KW Chaparonin; ATP-binding; Multigene family.  
FT INIT MET 0  
FT INIT MET 0  
FT INIT MET 0  
SQ SEQUENCE 476 AA; 50525 MW; 760F81793F4E9D CRC64;

Query Match 100.0%; Score 87; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPITNDG 16  
|||||

DB 36 VLEKKMGAPTTNDG 51

RESULT 2

CH60\_TSUTY STANDARD; PRT; 539 AA.

AC P97086; 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (heat shock protein 60).

GN GROEL OR GROEL OR HSP60.

OS *Taukamuraella tyrosinoseolvens*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Taukamuraellaceae*; *Taukamuraella*.

OX NCBI\_TaxID=57704;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IMWB D-1411;

RA Zimmermann O., Pinkenburg O., Koehnel H.G.;

RT "Taukamuraella tyrosinoseolvens sp. nov. hsp60 gene for heat shock protein 60."

RU Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.

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CC -----

DR EMBL: U90204; AABA9990.1; -

DR HSP60; P06139; 1GRU.

DR HAMAP: MF\_00600; -; 1.

DR InterPro: IPR001844; Chaperonin Cpn60.

DR InterPro: IPR002423; Cpn60/TCF-1.

DR Pfam: PF00118; Cpn60 TCF1.1.

DR PRINTS: PRO0298; CHAPERONIN60.

DR PRINTS: PRO0304; TCOMPLEXTCP1.

DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.

KW Chaperone; ATP-binding.

SV SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 539;

Best Local Similarity 100.0%; Pred. No. 4.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTNDG 16

DB 37 VLEKKMGAPTTNDG 52

RESULT 3

CH62\_MYCTU STANDARD; PRT; 539 AA.

AC P06806; Q48920; Q48931;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1998 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin 2 (protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (heat shock protein 65) (Cell wall protein A) (Antigen A).

GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.

OS *Mycobacterium tuberculosis*, and *Mycobacterium bovis*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Mycobacteriaceae*; *Mycobacterium*.

OX NCBI\_TaxID=1773, 1765;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=Erasmus;

RX MEDLINE=67137260; PubMed=3029018;

RA Shinnick T.M.;

RT "The 65-kilodalton antigen of *Mycobacterium tuberculosis*."

RU J. Bacteriol. 169:1080-1088(1987).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagsle K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulten J.E., Taylor K., Whitehead S., Barrell B.G.;

RA "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence."

RU Nature 393:537-544(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;

RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains."

RU Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=67193155; PubMed=3553003;

RA Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Berwald L.G., Tiesjema R.H., van Embden J.D.A.;

RT "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of *Mycobacterium bovis* BCG expressed in *Escherichia coli* K-12."

RU Infect. Immun. 55:1466-1475(1987).

RN [5]

RP SEQUENCE OF 45-195 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;

RA Ros C., Belak K.;

RU Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE OF 63-182 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TWC 410, and TWC 1024;

RX MEDLINE=95150784; PubMed=7848059;

RA Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M., Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Clarridge J.E., Kreiswirth B.N., Musser J.M.;

RT "Rapid *Mycobacterium* species assignment and unambiguous identification of mutations associated with antitubercular resistance in *Mycobacterium tuberculosis* by automated DNA sequencing."

RU Arch. Pathol. Lab. Med. 119:131-138(1995).

RN [7]

RP SEQUENCE OF 64-177 FROM N.A.

RC SPECIES=M.tuberculosis;

RX MEDLINE=95214306; PubMed=7699930;

RA Hatake R., Ueno I., Kawakami Y., Furutawari C., Furuhata K., Katsuyama T.;

RT "Detection and identification of *Mycobacterium* by PCR-RFLP method."

RU Risho Boyei 43:115-161(1995).

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 25.7778 Seconds  
(without alignments)  
160.171 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87  
Sequence: 1 VLEKXWGPITNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_plant:\*
- 10: sp\_virus:\*
- 11: sp\_vertebrate:\*
- 12: sp\_vertebrate:\*
- 13: sp\_vertebrate:\*
- 14: sp\_vertebrate:\*
- 15: sp\_vertebrate:\*
- 16: sp\_vertebrate:\*
- 17: sp\_vertebrate:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	59	2	Q9EMD1 streptomycin
2	87	100.0	61	2	Q9EMD1 streptomycin
3	87	100.0	539	2	P97086 tsukamureli
4	87	100.0	540	2	Q9AF55 tsukamureli
5	87	100.0	541	2	Q93Q12 corynebacte
6	87	100.0	541	2	Q9AF55 corynebacte
7	87	100.0	541	2	Q9KGM1 corynebacte
8	87	100.0	542	2	Q9AF55 corynebacte
9	87	100.0	548	2	Q9AF55 corynebacte
10	87	100.0	548	2	Q9AF55 corynebacte
11	87	100.0	548	2	Q9AF55 corynebacte
12	87	100.0	548	2	Q9AF55 corynebacte
13	87	100.0	549	2	Q9AF55 corynebacte
14	87	100.0	549	2	Q9AF55 corynebacte
15	87	100.0	549	2	Q9AF55 corynebacte
16	87	100.0	549	2	Q9AF55 corynebacte

17	70	80.5	537	2	Q9K171 parascardov
18	70	80.5	541	2	Q9K157 gaidnerella
19	69	79.3	537	2	Q9M78 bifidobacte
20	69	79.3	538	2	Q9M78 bifidobacte
21	69	79.3	541	16	Q9M78 bifidobacte
22	69	79.3	541	16	Q9M78 bifidobacte
23	68	78.2	539	2	Q9K20 bacillus st
24	68	78.2	539	2	Q9K20 bacillus st
25	68	78.2	543	2	Q9K20 bacillus st
26	68	78.2	543	2	Q9K20 bacillus st
27	67	77.0	543	2	Q9K20 bacillus st
28	67	77.0	543	2	Q9K20 bacillus st
29	66	75.9	352	2	Q9K20 bacillus st
30	66	75.9	352	2	Q9K20 bacillus st
31	66	75.9	352	2	Q9K20 bacillus st
32	66	75.9	352	2	Q9K20 bacillus st
33	66	75.9	352	2	Q9K20 bacillus st
34	66	75.9	352	2	Q9K20 bacillus st
35	66	75.9	352	2	Q9K20 bacillus st
36	66	75.9	352	2	Q9K20 bacillus st
37	66	75.9	352	2	Q9K20 bacillus st
38	66	75.9	352	2	Q9K20 bacillus st
39	66	75.9	352	2	Q9K20 bacillus st
40	66	75.9	352	2	Q9K20 bacillus st
41	66	75.9	352	2	Q9K20 bacillus st
42	66	75.9	352	2	Q9K20 bacillus st
43	66	75.9	352	2	Q9K20 bacillus st
44	66	75.9	352	2	Q9K20 bacillus st
45	66	75.9	352	2	Q9K20 bacillus st

## ALIGNMENTS

Q9EMD1	PRELIMINARY	PRT	59 AA.
AC Q9EMD1	01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT 01-MAR-2002	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Heat-shock protein (Fragment)		
GN	GROEL2		
OS	Streptomyces coelicolor		
OC	Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;		
OX	Streptomyces; Streptomycetaceae; Streptomyces		
NCBI_TaxID=1902;			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=J802;		
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;		
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces		
RT	antibiotic biosynthesis."		
RT	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ250536; CAC19351.1; -		
DR	HSSP; P06139; 1AON.		
DR	InterPro; IPR002423; Cpn60/TCF-1;		
DR	Pfam; PF00118; cpm60 TCPI; 1		
KW	PRINTS; PR00304; TCOMPLEXTCPI.		
FT	ATP-binding; Chaperone.		
FT	NON_TER		
FT	SEQUENCE 59 AA; 6407 MW; E7B24199B7DB68FA CRC64;		
Query Match	100.0%; Score 87; DB 2; Length 59;		
Best Local Similarity	100.0%; Pred. No. 5e-07; Indels 0;		
Matches	16; Conservative 0; Mismatches 0; Gaps 0;		
Q9	1 VLEKXWGPITNDG 16		
DB	37 VLEKXWGPITNDG 52		
RESULT 2			

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Q9EUR7          PRELIMINARY;      PRT;      61 AA.
ID Q9EUR7;
AC Q9EUR7;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Heat-shock protein (Fragment).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OK NCBI_TaxId=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RL antibiotic biosynthesis."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1; 1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
KW ATP-binding; Chaperone.
FT NON TER 61
SQ SEQUENCE 61 AA; 6645 MW; D20095FF4199B7CA CRC64;

Query Match          100.0%; Score 87; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 3
P97086          PRELIMINARY;      PRT;      539 AA.
ID P97086;
AC P97086;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Tsukamurellaceae; Tsukamurella.
OK NCBI_TaxId=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMTB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
RT protein 60."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
RL PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
RL CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00236; CHAPERONIN_CPN60; 1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49BF7C CRC64;

Query Match          100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 5
Q93012          PRELIMINARY;      PRT;      541 AA.
ID Q93012;
AC Q93012;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Nocardiaceae; Rhodococcus.
OK NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match          100.0%; Score 87; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 4
Q9AFAS          PRELIMINARY;      PRT;      540 AA.
ID Q9AFAS;
AC Q9AFAS;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Tsukamurellaceae; Tsukamurella.
OK NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
RL PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
RL CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF32578; AKI18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00236; CHAPERONIN_CPN60; 1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49BF7C CRC64;

Query Match          100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 5
Q93012          PRELIMINARY;      PRT;      541 AA.
ID Q93012;
AC Q93012;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Nocardiaceae; Rhodococcus.
OK NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 31.4074 Seconds  
(without alignments)  
80.861 Million cell updates/sec

Title: US-09-847-637B-3  
Perfect score: 87  
Sequence: 1 VVLEKKWGAPTTNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	21	AAV93330
2	87	100.0	16	23	AAU99965
3	87	100.0	22	21	AAV93328
4	87	100.0	215	19	AAW60145
5	87	100.0	215	20	AAV14892
6	87	100.0	215	23	ABR73498
7	87	100.0	295	22	AAH31615
8	87	100.0	523	19	AAW60144
9	87	100.0	523	20	AAV14891

10	87	100.0	523	23	ABR73497	M. vaccae GroEL, hom
11	87	100.0	539	20	AAV23919	Amino acid sequenc
12	87	100.0	540	16	AAH81351	Sequence of Mycob
13	87	100.0	540	16	AAH81610	Mycobacterium tube
14	87	100.0	540	18	AAW32100	Mycobacterium sp. h
15	87	100.0	540	19	AAW44702	Mycobacterium tube
16	87	100.0	540	20	AAV23911	Amino acid sequenc
17	87	100.0	540	21	AAV33332	Amino acid sequenc
18	87	100.0	540	22	AAH11755	Mycobacterium tube
19	87	100.0	540	22	AAH81118	Mycobacterium tube
20	87	100.0	540	22	AAH31606	Amino acid sequenc
21	87	100.0	540	23	AAU76510	M. leprae 65kDa st
22	87	100.0	540	23	AAU76511	M. tuberculosis 65
23	87	100.0	540	23	AAU76193	Mycobacterium lepr
24	87	100.0	540	23	AAU76194	Mycobacterium tube
25	87	100.0	540	23	AAW50750	Mycobacterium tube
26	87	100.0	540	24	ABG74587	M. leprae 65kDa st
27	87	100.0	540	24	ABG74588	M. tuberculosis 65
28	87	100.0	541	16	AAH67384	M. leprae GroEL, g
29	87	100.0	541	20	AAV14909	Amino acid sequenc
30	87	100.0	541	20	AAV23910	Amino acid sequenc
31	87	100.0	541	20	AAV23913	Amino acid sequenc
32	87	100.0	541	23	ABR73515	M. vaccae GroEL, hom
33	87	100.0	544	18	AAW32059	Mycobacteria sp. h
34	87	100.0	560	9	AAH80215	Sequence of Mycob
35	87	100.0	572	11	AAH04716	Amino acid sequenc
36	87	100.0	573	11	AAH04715	Amino acid sequenc
37	87	100.0	573	16	AAH04765	M. leprae 65 kDa p
38	87	100.0	573	16	AAH04766	M. tuberculosis 65
39	87	100.0	588	9	AAH80364	M. leprae 65kD ant
40	87	100.0	638	21	AAH803790	Heat shock protein
41	87	100.0	639	22	AAH31609	Amino acid sequenc
42	87	100.0	648	22	AAH31614	Amino acid sequenc
43	87	100.0	690	23	ABG70777	BCG Hsp65/mutant H
44	87	100.0	709	23	ABG70776	BCG Hsp65/mutant H
45	87	100.0	724	23	ABG70778	BCG Hsp65/mutant H

#### ALIGNMENTS

##### RESULT 1

AAV93330 standard; peptide: 16 AA.

ID AAV93330;

AC AAV93330;

DT 04-SEP-2000 (first entry)

XX Amino acid sequence of an epitope of heat shock protein 60.

DE Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;

KW inflammatory disorder; arthritis.

XX Mycobacterium tuberculosis.

OS W0200027870-A1.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-IL00595.

XX 05-NOV-1998; 98US-0107213.

XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX Naparstek Y, Umanaky R, Kaashi Y;

XX WPI; 2000-376486/32.

XX Peptide having a defined sequence is used in vaccines for conferring

PT immunity against autoimmune disease or inflammatory disorders,

PT especially arthritis

XX Claim 3; Page 7; 58pp; English.

PS The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKWGAPITNDG 16  
 Db 1 VVLEKKWGAPITNDG 16

RESULT 2  
 AAU99965

ID AAU99965 standard; Peptide; 16 AA.

AC AAU99965;

DT 07-OCT-2002 (first entry)

DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.

XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 KW autoimmune disease; infectious disease; graft rejection; type I diabetes;  
 KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 KW arteriosclerosis.

OS Mycobacterium tuberculosis.

PN WO200248312-A2.

PD 20-JUN-2002.

PF 11-DEC-2001; 2001WO-1101144.

PR 11-DEC-2000; 2000IL-0140233.

PA (PEPT-) PEPTOR LTD.

PI Elias D, Avron A, Senderowitz H;

DR WPI; 2002-557613/59.

PT New backbone cyclised peptide analog of heat shock protein useful in  
 the treatment of e.g. autoimmune disease -

PS Claim 5; Page 42; 50pp; English.

XX The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKWGAPITNDG 16  
 Db 1 VVLEKKWGAPITNDG 16

RESULT 3  
 AAU93328  
 ID AAU93328 standard; peptide; 22 AA.

AC AAU93328;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

XX Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KW inflammatory disorder; arthritis.

OS Mycobacterium tuberculosis.

PN WO20027870-A1.

PD 18-MAY-2000.

PF 04-NOV-1999; 99WO-1100595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PI Naparstek Y, Ulimansky R, Kasht Y;

DR WPI; 2000-376486/32.

PT Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -

PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX Sequence 22 AA;

Query Match 100.0%; Score 87; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKKWGAPITNDG 16  
 Db 7 VVLEKKWGAPITNDG 22

RESULT 4  
 AAU60145  
 ID AAU60145 standard; Protein; 215 AA.

AC AAU60145;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27A sequence.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
 KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KW Mycobacteria infection; vaccine; cancer.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 30, 2003, 16:09:39 ; Search time 21.9259 Seconds  
(without alignments)  
145.229 Million cell updates/sec

Title: US-09-847-637B-3  
Sequence: 1 VLEKKWGAPITINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*  
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16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	US-09-847-637B-3	Sequence 3, Appl1
2	87	100.0	22	US-09-847-637B-1	Sequence 1, Appl1
3	87	100.0	215	US-09-880-505-117	Sequence 117, Appl
4	87	100.0	215	US-10-205-979-41	Sequence 41, Appl
5	87	100.0	215	US-10-051-643-117	Sequence 117, Appl
6	87	100.0	295	US-10-267-311-33	Sequence 33, Appl
7	87	100.0	523	US-09-880-505-114	Sequence 114, Appl
8	87	100.0	523	US-10-051-643-114	Sequence 114, Appl
9	87	100.0	540	US-09-847-637B-6	Sequence 6, Appl1
10	87	100.0	540	US-09-712-363-169	Sequence 169, Appl
11	87	100.0	540	US-10-267-311-4	Sequence 4, Appl1
12	87	100.0	540	US-10-046-649-3	Sequence 3, Appl1
13	87	100.0	540	US-10-046-649-4	Sequence 4, Appl1
14	87	100.0	541	US-09-880-505-160	Sequence 160, Appl
15	87	100.0	541	US-10-205-979-40	Sequence 40, Appl

16	87	100.0	541	US-10-051-643-160	Sequence 160, Appl
17	87	100.0	541	US-10-156-761-11465	Sequence 11465, A
18	87	100.0	576	US-10-369-493-8322	Sequence 8322, Ap
19	87	100.0	639	US-10-267-311-17	Sequence 17, Appl
20	87	100.0	648	US-10-267-311-29	Sequence 29, Appl
21	87	100.0	690	US-10-068-059-10	Sequence 10, Appl
22	87	100.0	709	US-10-068-059-8	Sequence 8, Appl1
23	87	100.0	724	US-10-068-059-12	Sequence 12, Appl
24	87	100.0	746	US-10-068-059-6	Sequence 6, Appl1
25	87	100.0	948	US-10-267-311-21	Sequence 21, Appl
26	81	93.1	548	US-09-738-626-6486	Sequence 6486, Ap
27	77	88.5	538	US-10-369-493-2950	Sequence 2950, Ap
28	72	82.8	542	US-10-156-761-12526	Sequence 12526, A
29	68	78.2	544	US-10-369-493-17132	Sequence 17132, A
30	68	78.2	544	US-10-369-493-23094	Sequence 23094, A
31	66	75.9	521	US-10-369-493-9597	Sequence 9597, Ap
32	66	75.9	540	US-10-369-493-15838	Sequence 15838, A
33	66	75.9	544	US-10-369-493-15468	Sequence 15468, A
34	66	75.9	544	US-10-369-493-16217	Sequence 16217, A
35	66	75.9	544	US-10-369-493-20276	Sequence 20276, A
36	66	75.9	548	US-10-369-493-513	Sequence 513, App
37	65	74.7	544	US-10-369-493-20873	Sequence 20873, A
38	65	74.7	545	US-10-228-167A-2	Sequence 2, Appl1
39	65	74.7	545	US-10-369-493-19756	Sequence 19756, A
40	64	73.6	547	US-10-369-493-10014	Sequence 10014, A
41	63	72.4	547	US-10-046-649-2	Sequence 2, Appl1
42	63	72.4	548	US-09-415-849-1	Sequence 1, Appl1
43	63	72.4	548	US-09-276-455-10	Sequence 10, Appl
44	63	72.4	551	US-10-369-493-20184	Sequence 20184, A
45	63	72.4	641	US-10-267-311-51	Sequence 51, Appl

## ALIGNMENTS

RESULT 1  
US-09-847-637B-3  
Sequence 3, Application US/09847637B  
Patent No. US20020150586A1  
GENERAL INFORMATION:  
APPLICANT: Naparstek, Yaakov  
APPLICANT: Umanetsky, Rina  
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USBS THEREOF  
FILE REFERENCE: 13125-002001  
CURRENT APPLICATION NUMBER: US/09/847,637B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: PCT/IL99/00595  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,213  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-847-637B-3  
Query Match 100.0%; Score 87; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLEKKWGAPITINDG 16  
DB 1 VLEKKWGAPITINDG 16  
RESULT 2  
US-09-847-637B-1  
Sequence 1, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Umanaky, Rina
; APPLICANT: Kash, Yechazkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847, 637B
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-1

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Query Match      100.0%; Score 87; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLEKKKGAPTTNDG 16
DB      7 VLEKKKGAPTTNDG 22

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RESULT 3
US-09-880-505-117
; Sequence 117, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Rose
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880, 505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-117

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Query Match      100.0%; Score 87; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLEKKKGAPTTNDG 16
DB      37 VLEKKKGAPTTNDG 52

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RESULT 4
US-10-205-979-41
; Sequence 41, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.

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; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205, 979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
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US-10-205-979-41

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Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLEKKKGAPTTNDG 16
DB      37 VLEKKKGAPTTNDG 52

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RESULT 5
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; Sequence 117, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-117

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Query Match      100.0%; Score 87; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLEKKKGAPTTNDG 16
DB      37 VLEKKKGAPTTNDG 52

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RESULT 6
US-10-267-311-33
; Sequence 33, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267, 311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

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(without alignments)  
60.126 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VLEKKMGAPTITNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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20	87	100.0	540	5 PCT-US94-06362-3	Sequence 3, App
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22	87	100.0	541	2 US-08-467-822-34	Sequence 34, App
23	87	100.0	541	2 US-08-447-154-19	Sequence 19, App
24	87	100.0	541	2 US-08-997-080-160	Sequence 160, App
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26	87	100.0	541	3 US-09-095-855-160	Sequence 160, App
27	87	100.0	541	3 US-08-432-697-34	Sequence 34, App

28	87	100.0	541	3 US-08-466-248-34	Sequence 34, App
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31	87	100.0	639	4 US-09-613-303-17	Sequence 17, App
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33	87	100.0	948	4 US-09-613-303-21	Sequence 21, App
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39	63	72.4	547	4 US-08-336-251-2	Sequence 2, App
40	63	72.4	547	4 US-09-468-041-2	Sequence 2, App
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42	63	72.4	548	2 US-08-467-822-32	Sequence 32, App
43	63	72.4	548	3 US-09-472-971-3	Sequence 3, App
44	63	72.4	548	3 US-08-432-697-32	Sequence 32, App
45	63	72.4	548	3 US-08-466-248-32	Sequence 32, App

## ALIGNMENTS

RESULT 1  
US-08-997-080-117  
; Sequence 117, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-997-080-117  
; Query Match 100.0%; Score 87; DB 2; Length 215;  
; Best Local Similarity 100.0%; Pred. No. 3e-07;  
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; 1 VLEKKMGAPTITNDG 16

DB 37 VLEKKWGAPTINDG 52

RESULT 2  
US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiayama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 87; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKWGAPTINDG 16

DB 37 VLEKKWGAPTINDG 52

RESULT 3  
US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross  
TITLE OF INVENTION: Compounds and Methods for  
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 87; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKWGAPTINDG 16

DB 37 VLEKKWGAPTINDG 52

RESULT 4  
US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 117

LENGTH: 215

TYPE: PRT

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 30, 2003, 16:21:30 / Search time 21 Seconds  
(without alignments)  
100.748 Million cell updates/sec

Title: US-09-847-637B-1  
Perfect score: 122  
Sequence: 1 GPKGRNVLEKKWGAFLITNDG 22

Scoring table: BLOSUM62  
Gapop 10.0, Gapept 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 4264

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR 76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	24.6	18	1	MTDFBC
2	29	23.8	17	2	A37823
3	28	23.0	21	2	S03986
4	28	23.0	22	2	A45913
5	27	22.1	18	1	MTROB
6	27	22.1	21	2	A42762
7	27	22.1	21	2	S62893
8	27	22.1	22	2	A12846
9	26	21.3	14	2	I54945
10	26	21.3	15	2	PI631
11	26	21.3	16	2	E58501
12	26	21.3	17	2	B53113
13	26	21.3	19	2	FX0062
14	25	20.5	13	1	MTCMAD
15	25	20.5	13	1	MTMOAD
16	25	20.5	17	2	S03531
17	25	20.5	18	1	DRUFED
18	25	20.5	18	1	A29558
19	25	20.5	20	2	A26488
20	25	20.5	21	2	S33287
21	25	20.5	21	2	PC1310
22	24	20.1	17	2	PH1357
23	24	19.7	15	2	UN0730
24	24	19.7	20	2	PQ0071
25	24	19.7	21	2	I54268
26	23.5	19.3	20	2	S29635
27	23	18.9	11	2	A34243
28	23	18.9	15	2	PH0760
29	23	18.9	22	2	UC0009

30	23	18.9	22	2	A28563	hemoglobin chain I
31	22.5	18.4	20	2	P42762	proteasome endopep
32	22.5	18.4	20	2	PH1380	alpha-amylase (EC
33	22	18.0	8	2	A31570	angiotensin-conver
34	22	18.0	13	2	G83988	hypothetical prote
35	22	18.0	17	2	S77834	DNA-directed RNA p
36	22	18.0	18	2	G84114	hypothetical prote
37	22	18.0	20	2	S29636	hypothetical prote
38	22	18.0	20	2	S10876	jacalin beca-I cha
39	22	18.0	21	2	S71602	hypothetical prote
40	22	18.0	22	2	PQ0070	recombinational prot
41	21.5	17.6	17	2	S24570	T-cell receptor be
42	21.5	17.6	20	2	S03987	Ig heavy chain J r
43	21	17.2	11	2	S09074	agglutinin beta-2
44	21	17.2	11	2	YHRT	cytochrome P450-4b
45	21	17.2	11	2	YHRT	morphogenetic neur

## ALIGNMENTS

RESULT 1  
MTDFBC  
melanotropin beta - smaller spotted catshark  
C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 23-Aug-1996  
C/Accession: A01470  
R/Love, R.M.; Pickering, B.T.  
Gen. Comp. Endocrinol. 24, 398-404, 1974  
A/Title: A beta-MSH in the pituitary gland of the spotted dogfish (Scyliorhinus canicula)  
A/Reference number: A01470; MUID:75113445; PMID:4452470  
A/Accession: A01470  
A/Molecule type: protein  
A/Residues: 1-18 <LOV>  
C/Superfamily: corticotropin-lipotropin  
C/Keywords: hormone

Query Match 24.6%; Score 30; DB 1; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KWGAP 16  
DB 11 RWGAP 15

RESULT 2  
A37823  
dihydroliipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 05-May-2000  
C/Accession: A37823  
R/Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.  
J. Biol. Chem. 265, 14512-14517, 1990  
A/Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon selec  
A/Reference number: A37823; MUID:90354445; PMID:2167319  
A/Accession: A37823  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-17 <RAH>  
C/Keywords: acyltransferase; coenzyme A

Query Match 23.8%; Score 29; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGR 5  
DB 1 GPKGR 5

RESULT 3  
S03986

agglutinin beta-1 chain - Oeage orange  
 C/Species: Maciura pomifera (Oeage orange)  
 C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 01-Aug-1997  
 C/Accession: S03986; S03988  
 R/Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.  
 Arch. Biochem. Biophys. 270, 596-603, 1989  
 A/Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia and M  
 A/Reference number: S03983; MUID:89206218; PMID:2705782  
 A/Accession: S03986  
 A/Molecule type: protein  
 A/Residues: 1-21 <Y0U>  
 A/Note: beta-1 form  
 A/Accession: S03988  
 A/Molecule type: protein  
 A/Residues: 2-21 <Y02>  
 A/Note: beta-3 form

Query Match 23.0%; Score 28; DB 2; Length 21;  
 Best Local Similarity 33.3%; Pred. No. 9.2e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VLEKKWGAPITN 20  
 |||:::|:|:|  
 Db 2 GPNKGSQSTIVGFWG-DVITN 21

RESULT 4  
 A45913  
 plantaricin A - Lactobacillus plantarum  
 C/Species: Lactobacillus plantarum  
 C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 12-Sep-1997  
 C/Accession: A45913  
 R/Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.  
 submitted to the Protein Sequence Database, April 1993  
 A/Reference number: A45913  
 A/Accession: A45913  
 A/Status: preliminary  
 A/Title: Induction of proteins in response to cold acclimation of rainbow trout cells.  
 A/Molecule type: protein  
 A/Residues: 1-22 <NIS>  
 C/Keywords: antibiotic; bacteriocin

Query Match 23.0%; Score 28; DB 2; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 LEKKWG 14  
 |||||  
 Db 17 LFRKKG 22

RESULT 5  
 MTHOB  
 melanotropin beta - horse  
 C/Species: Equus caballus (domestic horse)  
 C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 23-Aug-1996  
 C/Accession: A01467  
 R/Dixon, J.S.; Li, C.H.  
 Gen. Comp. Endocrinol. 1, 161-169, 1961  
 A/Title: The isolation and structure of beta-melanocyte-stimulating hormone from horse p  
 A/Reference number: A01467  
 A/Accession: A01467  
 A/Molecule type: protein  
 A/Residues: 1-18 <DIX>  
 C/Superfamily: corticotropin-11potropin  
 C/Keywords: hormone

Query Match 22.1%; Score 27; DB 1; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 KWGAP 16  
 |||||  
 Db 11 RWGSP 15

RESULT 6  
 A42762  
 proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003  
 C/Accession: A42762  
 R/Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
 Biochemistry 31, 7347-7355, 1992  
 A/Title: Identification and localization of a cysteinyl residue critical for the trypsi  
 A/Reference number: A42762; MUID:92378961; PMID:1510924  
 A/Accession: A42762  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-21 <DIC>  
 A/Note: sequence extracted from NCBI backbone (NCBIP:112172)  
 C/Superfamily: multicatalytic endopeptidase complex chain C9  
 C/Keywords: hydrolase

Query Match 22.1%; Score 27; DB 2; Length 21;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 GAPITND 21  
 |||:|:|  
 Db 8 GCPWVITD 15

RESULT 7  
 S62893  
 cold-inducible protein, 70K - rainbow trout (fragment)  
 C/Species: Oncorhynchus mykiss (rainbow trout)  
 C/Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 24-Jul-1997  
 C/Accession: S62893  
 R/Yamashita, M.; Ojima, N.; Sakamoto, T.  
 FEBS Lett. 382, 261-264, 1996  
 A/Title: Induction of proteins in response to cold acclimation of rainbow trout cells.  
 A/Reference number: S62893; MUID:96184500; PMID:8605981  
 A/Accession: S62893  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-21 <YAM>

Query Match 22.1%; Score 27; DB 2; Length 21;  
 Best Local Similarity 46.7%; Pred. No. 1.3e+03;  
 Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 GPKGRNVLEKKWGCA 15  
 |||:|:|  
 Db 6 GPKGTGKML--IWGA 18

RESULT 8  
 A12846  
 hypochlorite protein Atu2202 [imported] - Agrobacterium tumefaciens (strain C58, Dupont  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
 C/Accession: A12846  
 R/Wood, D.W.; Sebda, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCle  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm  
 ster, E.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; MUID:21608550; PMID:11743193  
 A/Accession: A12846  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-22 <KUR>  
 A/Cross-references: GB:AB00668; PIDN:AAI43191.1; PTD:917740671; GSPDB:GN00186  
 A/Experimental source: strain C58 (Dupont)



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:12:10 ; Search time 11 Seconds  
(without alignments)

94.053 Million cell updates/sec

Title: US-09-847-637B-1

Sequence: 1 GPKRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1361

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	25.4	19	1	CH10_CLOPA
2	30	24.6	18	1	MLB_SCYCA
3	28	23.0	20	1	LEC3_MACRO
4	28	23.0	21	1	LEC1_MACRO
5	27	22.1	17	1	FLA2_BARBA
6	27	22.1	18	1	MLB_HORSE
7	25	20.5	13	1	MLA_ANOCA
8	25	20.5	13	1	MLA_CAMDR
9	25	20.5	15	1	UNO1_PINPS
10	25	20.5	18	1	DRPH_UCAPU
11	24	19.7	21	1	LEC2_ARTIN
12	23	18.9	11	1	ASL2_BACSE
13	23	18.9	20	1	LEC1_ARTIN
14	23	18.9	21	1	UAP2_RANTA
15	23	18.9	22	1	HGJ2_FASHE
16	23	18.9	22	1	PA2_DABRU
17	22	18.0	8	1	ACI_THUL
18	22	18.0	10	1	UHA3_HUMAN
19	22	18.0	20	1	LEC3_ARTIN
20	22	18.0	22	1	BS23_SERPL
21	22	18.0	22	1	TL11_SPIOL
22	21.5	17.6	20	1	LEC2_MACRO
23	21	17.2	11	1	MORN_HUMAN
24	21	17.2	20	1	VAR9_BORPE
25	21	17.2	21	1	SC1B_BPTS
26	20	16.4	13	1	LIGA_TRAVE
27	20	16.4	13	1	UNO2_PINPS
28	20	16.4	14	1	MCRX_METTM
29	20	16.4	16	1	MLB_SQUAC
30	20	16.4	18	1	AGI_EUPCH
31	20	16.4	19	1	AB27_CYPCA
32	20	16.4	19	1	PGK_EACCE
33	20	16.4	20	1	TPX_CLOPA

34	20	16.4	22	1	DEP1_SPIOL	P81572	epinacia o1
35	19	15.6	9	1	TRK1_LOCM1	P16223	locusta mig
36	19	15.6	10	1	BPE2_BOTUA	P01022	botrrops ja
37	19	15.6	11	1	CEP1_ACHFU	P22790	achalina fu
38	19	15.6	12	1	UP01_CAEEL	P55954	caenothabdi
39	19	15.6	13	1	IDHP_RAT	P56574	ratius norv
40	19	15.6	13	1	LIGB_TRAVE	P20012	trameles ve
41	19	15.6	14	1	SAP2_ARBPV	P11760	arbecia pun
42	19	15.6	15	1	UC06_MAIZB	P80612	zea mays (m
43	19	15.6	16	1	MMPX_SOLTU	P80501	solanum tub
44	19	15.6	18	1	AGI_BUPMA	P33889	euphorbia m
45	19	15.6	20	1	PGK_CLOPA	P81346	clostridium

## ALIGNMENTS

```

RESULT 1
CH10_CLOPA          STANDARD; PRT; 19 AA.
ID_CH10_CLOPA
AC P81338;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 10 kDa chaperonin (Protein Cpn10) (GROS protein) (CP 31) (Fragment).
GN GROS OR GROS.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RL sequence analysis of proteins from Clostridium pasteurianum W5."
CC Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses
CC the ATPase activity of the latter.
CC -1- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GROS CHAPERONIN FAMILY.
DR HAMAP; MF 00580; -; 1.
DR InterPro; IPR001476; Chaperin_Cpn10.
DR Pfam; PF00166; Cpn10; 1.
DR PROSITE; PS00681; CHAPERONINS_CPN10; PARTIAL.
KW Chaperone.
KW NON_TER
SQ SEQUENCE 19 AA; 2026 MW; 7D6B9BD414E60A60 CRC64;
FT
FT NON_TER
Query Match 25.4%; Score 31; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKGRNVVLEK 11
DB 5 FLGDNVVLEK 14
RESULT 2
MLB_SCYCA          STANDARD; PRT; 18 AA.
ID_MLB_SCYCA
AC P01206;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocytropin beta (Beta-MSH).
OS Melanocytropin canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryotes; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.

```

OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=7513445; PubMed=4452470;  
 RA Love R.M., Pickering B.T.;  
 RT "A beta-MSH in the pituitary gland of the spotted dogfish (Scyliorhinus canicula): isolation and structure.";  
 RL Gen. Comp. Endocrinol. 24:398-404(1974).  
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
 DR PIR; A01470; MTDIBC.  
 KW Hormone.  
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DP4 CRC64;  
 QY  
 DB 12 KMGAP 16  
 11 RMGAP 15  
 Query Match 24.6%; Score 30; DB 1; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 LEC3\_MACPO STANDARD; PRT; 20 AA.  
 ID LEC3\_MACPO  
 AC P18677;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Agglutinin beta-3 chain (MPA).  
 OS MacLura pomifera (Osage orange).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Moraceae; MacLura.  
 OX NCBI\_TaxID=3496;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RX MEDLINE=89206218; PubMed=2705782;  
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
 RT "Homology of the D-galactose-specific lectins from Artocarpus integrifolia and MacLura pomifera and the role of an unusual small polypeptide subunit."  
 RL Arch. Biochem. Biophys. 270:596-603(1989).  
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN STRUCTURE GAL-BETA1-3-GALNAC.  
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
 DR HSSP; P18676; IJOT.  
 KW Lectin.  
 SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;  
 QY  
 DB 1 GPKGRN-VLEKKWGAPITN 20  
 1 GPNKGSOSIIVGPMG-DRVTN 20  
 Query Match 23.0%; Score 28; DB 1; Length 20;  
 Best Local Similarity 33.3%; Pred. No. 5.3e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

RESULT 4  
 LEC1\_MACPO STANDARD; PRT; 21 AA.  
 ID LEC1\_MACPO  
 AC P18675;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Agglutinin beta-1 chain (MPA).  
 OS MacLura pomifera (Osage orange).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Moraceae; MacLura.

OX NCBI\_TaxID=3496;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RX MEDLINE=89206218; PubMed=2705782;  
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
 RT "Homology of the D-galactose-specific lectins from Artocarpus integrifolia and MacLura pomifera and the role of an unusual small polypeptide subunit."  
 RL Arch. Biochem. Biophys. 270:596-603(1989).  
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN STRUCTURE GAL-BETA1-3-GALNAC.  
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
 DR PIR; S03986; S03986.  
 DR HSSP; P18676; IJOT.  
 KW Lectin.  
 SQ SEQUENCE 21 AA; 2196 MW; AA38811BCLBPD0E0 CRC64;  
 QY  
 DB 1 GPKGRN-VLEKKWGAPITN 20  
 2 GPNKGSOSIIVGPMG-DRVTN 21  
 Query Match 23.0%; Score 28; DB 1; Length 21;  
 Best Local Similarity 33.3%; Pred. No. 5.5e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

RESULT 5  
 FLA2\_BARBA STANDARD; PRT; 17 AA.  
 ID FLA2\_BARBA  
 AC P35634;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Flagellin: (Fragment).  
 OS Bartonella bacilliformis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bartonellaceae; Bartonella.  
 OX NCBI\_TaxID=774;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=KC584;  
 RX MEDLINE=94041612; PubMed=8225570;  
 RA Scherer D.C., Debucun-Connors I., Munnick M.F.;  
 RT "Characterization of Bartonella bacilliformis flagella and effect of anti-flagellin antibodies on invasion of human erythrocytes".  
 RL Infect. Immun. 61:4962-4971(1993).  
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA. FLAGELLA ARE AN IMPORTANT COMPONENT IN THE INVASIVENESS OF B. BACILLIFORMIS.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.  
 KW Flagella.  
 DR NON\_TER  
 SQ SEQUENCE 17 AA; 1746 MW; BA24BE6177CDB8 CRC64;  
 QY  
 DB 14 GAPITND 21  
 1 GAAILTND 8  
 Query Match 22.1%; Score 27; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 6.4e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 6  
 MLB\_HORSE STANDARD; PRT; 18 AA.  
 ID MLB\_HORSE  
 AC P01202;  
 DT 21-JUN-1986 (Rel. 01, Created)  
 DT 21-JUN-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin beta (Beta-MSH).

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:20:40 ; Search time 33 Seconds  
(without alignments)  
172.035 Million cell updates/sec

Title: US-09-847-637B-1  
Perfect score: 122  
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 8134

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_ivirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	28.7	18	6	Q9TRD8
2	27.5	22.5	16	4	Q9UCK9
3	27	22.1	17	4	Q9UPK4
4	27	22.1	21	13	Q9PRQ1
5	27	22.1	22	2	Q9AH71
6	27	22.1	22	13	Q9PRN2
7	27	22.1	22	16	Q8UDC5
8	26	21.3	14	2	Q47599
9	26	21.3	17	4	Q9R512
10	26	21.3	18	15	Q8NF84
11	26	21.3	18	15	Q73920
12	26	21.3	18	15	Q73921
13	25	20.5	10	11	Q70580
14	25	20.5	16	2	Q45530
15	25	20.5	17	4	Q9UC91
16	25	20.5	19	13	Q9PRN4

17	25	20.5	20	13	Q9PRN3	Q9PRN3 petromyzon
18	25	20.5	20	15	Q73918	Q73918 human immun
19	25	20.5	20	15	Q73917	Q73917 human immun
20	25	20.5	21	2	Q9AJG0	Q9AJG0 vibrio pela
21	25	20.5	21	5	Q9TMO5	Q9TMO5 tachypleus
22	25	20.5	22	11	Q9OMR6	Q9OMR6 mus sp. sgp
23	25	20.5	22	13	Q90ZV4	Q90ZV4 ralius lima
24	25	20.5	22	13	Q90ZV2	Q90ZV2 sarothrua
25	25	20.5	22	13	Q90ZV3	Q90ZV3 ralius long
26	25	20.5	22	13	Q910C6	Q910C6 gallinula c
27	24	19.7	10	4	Q9UNP2	Q9UNP2 homo sapien
28	24	19.7	15	2	Q9R4P5	Q9R4P5 brevidion
29	24	19.7	17	6	Q939P5	Q939P5 canis famli
30	24	19.7	18	6	Q9N1D5	Q9N1D5 canis famli
31	24	19.7	18	15	Q73487	Q73487 human immun
32	24	19.7	20	1	Q9UMM8	Q9UMM8 halobacteri
33	24	19.7	20	10	P83423	P83423 morus nigra
34	24	19.7	20	10	P83426	P83426 morus nigra
35	24	19.7	21	4	Q15965	Q15965 homo sapien
36	24	19.7	22	1	Q9UW19	Q9UW19 methanospir
37	23.5	19.3	20	10	Q9S8P1	Q9S8P1 atocarpus
38	23	18.9	11	15	Q83410	Q83410 mouse mamma
39	23	18.9	13	15	Q85645	Q85645 mouse mamma
40	23	18.9	16	2	Q10748	Q10748 clostridium
41	23	18.9	16	4	Q9UC18	Q9UC18 homo sapien
42	23	18.9	16	8	Q9T2V8	Q9T2V8 homo sapien
43	23	18.9	16	10	Q9S8D6	Q9S8D6 triticum ae
44	23	18.9	17	4	Q9UCF0	Q9UCF0 homo sapien
45	23	18.9	17	8	Q03888	Q03888 chlorogoniu

#### ALIGNMENTS

##### RESULT 1

Q9TRD8 PRELIMINARY; PRT; 18 AA.

AC Q9TRD8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE Chapteronin (Fragment).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCI\_Taxid=99986;

RN [1]

RP SEQUENCE.

RX MEDLINE=94089752; PubMed=7903455;

RA Rommelaere H., Van Troys M., Gao Y., Melki R., Cowan N.J.,

RA Vandekerckhove J., Ampe C.;

RT "Eukaryotic cytosolic chaperonin contains c-complex polypeptide 1 and

RT seven related subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979 (1993).

SO SEQUENCE 18 AA; 1884 MW; B608F6EB5A8A246 CRC64;

Query Match 28.7%; Score 35; DB 6; Length 18;

Best local similarity 46.7%; Pred. No. 1.5e+02;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Q9 8 VLEKKMGAPITINDG 22

DB 1 MMTDKDGVTVTNDG 15

##### RESULT 2

Q9UCK9 PRELIMINARY; PRT; 16 AA.

AC Q9UCK9; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)

DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93099171; PubMed=1463770;  
 RA Baba S., Takahashi T., Kasama T., Shiraawa H.;  
 RT "Identification of two novel amyloid A protein subunits coexisting in  
 an individual patient of AA-amyloidosis."  
 RL Biochim. Biophys. Acta 1180:195-200(1992).  
 CC -1- FUNCTION: MAJOR ACTE PHASE REACTANT. APOLOPROTEIN OF THE HDL  
 CC COMPLEX (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.  
 DR Interpro: IPR000096; Serum\_amyloid\_A.  
 KW Pfam: PF00277; SAA\_proteins; 1.  
 KM Acute phase; HDL.  
 SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 22.5%; Score 27.5; DB 4; Length 16;  
 Best Local Similarity 35.0%; Pred. No. 2e+03;  
 Matches 7; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

Oy 1 GPKGRNVLEKKGAPTTN 20  
 Db 2 GPGG-----AMAAEVISN 14

RESULT 3  
 O9UPK4 PRELIMINARY; PRT; 17 AA.  
 AC O9UPK4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE UCRY\_HUMAN (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lamerlin J.R., McCreedy P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez W., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,  
 RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
 RA Liu S., Altik C., Andreise T., Frankheim M., Antico-Keller G.,  
 RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
 RA Krommiller B., Ariellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
 RA Kobayashi A., Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of a 3.5 kb contig in human 19p13.3 containing a  
 RT serine protease gene cluster";  
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AC005321; AAC27374.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 2166 MW; B73A34E7EDB2B5D CRC64;

Query Match 22.1%; Score 27; DB 4; Length 17;  
 Best Local Similarity 46.2%; Pred. No. 2.6e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Oy 1 GPKGRNVLEKKG 13  
 Db 7 GPRYRELV--KNW 17

RESULT 4  
 O9PRO1 PRELIMINARY; PRT; 21 AA.  
 AC G9PRO1;

DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE 70 kDa cold acclimation-related protein (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Proteanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96184500; PubMed=8605981;  
 RA Yamaoka M., Ojima N., Sakamoto T.;  
 RT "Induction of proteins in response to cold acclimation of rainbow  
 RT trout cells";  
 RL FEBS Lett. 382:261-264(1996).  
 SQ SEQUENCE 21 AA; 2129 MW; FF68D74564917510 CRC64;

Query Match 22.1%; Score 27; DB 13; Length 21;  
 Best Local Similarity 46.7%; Pred. No. 3.2e+03;  
 Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Oy 1 GPKGRNVLEKKG 15  
 Db 6 GPGTGKML--IKQA 18

RESULT 5  
 O9AH71 PRELIMINARY; PRT; 22 AA.  
 AC O9AH71;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hmbr (Fragment).  
 GN Hmbr.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 NX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=44/76;  
 RX MEDLINE=21116988; PubMed=11179344;  
 RA Kahler C.M., Blum E., Miller Y.K., Ryan D., Popovic T., Stephens D.S.;  
 RT "xyl, an exchangeable genetic island in Neisseria meningitidis";  
 RL Infect. Immun. 69:1687-1696(2001).  
 DR EMBL: AF319527; AAK08019.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 22 AA; 2584 MW; F1BBBC6F2F3C2C49 CRC64;

Query Match 22.1%; Score 27; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 4 GRNVLEKKG 13  
 Db 11 GRNVAVSLFW 20

RESULT 6  
 O9PRN2 PRELIMINARY; PRT; 22 AA.  
 AC O9PRN2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Corticotropin, ACTH.  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 NX NCBI\_TaxID=7757;  
 RN [1]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:11:20 ; Search time 41 Seconds  
(without alignments)  
85.170 Million cell updates/sec

Title: US-09-847-637B-1  
Perfect score: 122  
Sequence: 1 GPKRRNVLEKMGAPRTINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 415757

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
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3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
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6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	22	21	AAV93328
2	90	73.8	16	21	AAV93329
3	90	73.8	16	23	AAU99964
4	87	71.3	16	18	AAW43458
5	87	71.3	16	21	AAV93330
6	87	71.3	16	23	AAU99965
7	83	68.0	15	17	AAV94779
8	83	68.0	15	18	AAW43457
9	82	67.2	16	17	AAV94780

10	70	57.4	15	18	AAW43459	Mycobacteria sp. h
11	65	53.3	15	17	AAV94781	Peptide from libra
12	59	48.4	20	21	AAV93331	Amino acid sequenc
13	59	48.4	20	23	AAU99966	Mycobacterium tube
14	57	46.7	16	17	AAV94778	Peptide from libra
15	57	46.7	16	18	AAW43456	Mycobacteria sp. h
16	47	38.5	11	22	AAV88272	Hsp-65 peptide epi
17	43	35.2	10	22	AAV88269	Hsp-65 peptide epi
18	42	34.4	20	19	AAV68089	Amino acids 1021-1
19	42	34.4	20	19	AAV68089	Tetanus toxin T-ce
20	39	32.0	15	23	AAE26843	Hsp-65 peptide epi
21	39	32.0	15	18	AAW43460	Myobacteria sp. h
22	39	32.0	17	17	AAV94777	Peptide from libra
23	39	32.0	17	18	AAW43455	Mycobacteria sp. h
24	36	29.5	20	22	ABG54657	Human liver peptid
25	36	29.5	20	22	ABG39610	Peptide #716 enco
26	36	29.5	20	22	AAV60314	Human brain expres
27	36	29.5	20	22	AAV72948	Human bone marrow
28	36	29.5	20	22	AAV33173	Peptide #7210 enco
29	36	29.5	20	23	ABG42785	Human peptide enco
30	36	28.7	16	16	AAV87908	Bovine lactoferrin
31	35	28.7	16	17	AAW10516	Lactoferrin derive
32	35	28.7	16	17	AAW10516	Lactoferrin derive
33	35	28.7	18	15	AAV69354	Bovine lactoferrin
34	35	28.7	18	17	AAW10515	Lactoferrin derive
35	35	28.7	19	23	AAU90668	Insulin/insulin-11
36	35	28.7	20	13	AAV21808	Anti microbial pep
37	35	28.7	20	13	AAV21809	Anti microbial pep
38	35	28.7	20	14	AAV44840	Lactoferrin relate
39	35	28.7	20	15	AAV48528	Lactoferrin derive
40	35	28.7	20	15	AAV48529	Lactoferrin derive
41	35	28.7	20	15	AAV57459	Lactoferrin derive
42	35	28.7	20	15	AAV57460	Lactoferrin derive
43	35	28.7	20	16	AAV84696	Bovine lactoferrin
44	35	28.7	20	16	AAV84697	Bovine lactoferrin
45	35	28.7	20	16	AAV80261	Anti-parasitic lac

#### ALIGNMENTS

RESULT 1  
AAV93328  
ID AAV93328 standard; peptide; 22 AA.  
XX AAV93328;  
AC  
XX  
DT 04-SEP-2000 (first entry)  
XX  
XX Amino acid sequence of an epitope of heat shock protein 60.  
DB  
XX Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX inflammatory disorder; arthritis.  
KW  
XX Mycobacterium tuberculosis.  
OS  
XX  
PN WO200027870-A1.  
XX  
XX 18-MAY-2000.  
PD  
XX  
XX 04-NOV-1999; 99WO-IL00595.  
PF  
XX  
XX 05-NOV-1998; 98US-0107213.  
PR  
XX  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA  
XX Naparstek Y, Ulanovsky R, Kaeshi Y;  
PI  
XX WPI; 2000-376486/32.  
DR  
XX  
XX Peptide having a defined sequence is used in vaccines for conferring  
PT immunity against autoimmune disease or inflammatory disorders,  
PT especially arthritis -

XX PS Claim 1; Page 7; 58pp; English.

CC CC The present sequence represents an epitope of the heat shock protein  
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
CC nucleic acid encoding it, are useful in vaccines for conferring  
CC immunity against autoimmune disease or inflammatory disorders,  
CC especially arthritis. The peptide may also be used to raise  
CC antibodies, which are then used for passive immunisation.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 122; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.9e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAPITINDG 22  
DB 1 GPKGRNVVLEKKMGAPITINDG 22

RESULT 2

AA93329 standard; peptide; 16 AA.

AC AAY93329;

DT 04-SEP-2000 (first entry)

XX DE Amino acid sequence of an epitope of heat shock protein 60.

XX KM Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX inflammatory disorder; arthritis.

XX OS Mycobacterium tuberculosis.

XX PN WO200027870-A1.

XX PD 18-MAY-2000.

XX PF 04-NOV-1999; 99WO-IL00595.

XX PR 05-NOV-1998; 98US-0107213.

XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX PI Naparstek Y, Ulanesky R, Kaehi Y;

XX DR WPI; 2000-376486/32.

XX PT Peptide having a defined sequence is used in vaccines for conferring  
XX PT immunity against autoimmune disease or inflammatory disorders,  
XX PT especially arthritis -

XX PS Claim 2; Page 7; 58pp; English.

CC CC The present sequence represents an epitope of the heat shock protein  
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
CC nucleic acid encoding it, are useful in vaccines for conferring  
CC immunity against autoimmune disease or inflammatory disorders,  
CC especially arthritis. The peptide may also be used to raise  
CC antibodies, which are then used for passive immunisation.

XX SQ Sequence 16 AA;

Query Match 73.8%; Score 90; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAP 16  
DB 1 GPKGRNVVLEKKMGAP 16

RESULT 3

AAU99964 standard; Peptide; 16 AA.

AC AAU99964;

DT 07-OCT-2002 (first entry)

XX DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.

XX XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
XX KW autoimmune disease; infectious disease; graft rejection; type I diabetes;  
XX KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
XX KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
XX KW arteriosclerosis.

XX OS Mycobacterium tuberculosis.

XX PN WO200248312-A2.

XX PD 20-JUN-2002.

XX PF 11-DEC-2001; 2001WO-IL01144.

XX PR 11-DEC-2000; 2000IL-0140233.

XX PA (PEPT-) PEPTOR LTD.

XX PI Elias D, Avron A, Senderowitz H;

XX DR WPI; 2002-557613/59.

XX PT New backbone cyclised peptide analog of heat shock protein useful in  
XX PT the treatment of e.g. autoimmune disease -

XX PS Claim 5; Page 42; 50pp; English.

CC CC The invention relates to backbone cyclised peptide analogues or  
CC antagonists of heat shock protein (hsp). The analogues and antagonists  
CC are useful in the treatment of chronic inflammatory disease, autoimmune  
CC disease, infectious disease and graft rejection, and for diagnosing  
CC autoimmune and inflammatory disease including juvenile rheumatoid  
CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
CC analogue of a heat shock protein.

XX SQ Sequence 16 AA;

Query Match 73.8%; Score 90; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAP 16

DB 1 GPKGRNVVLEKKMGAP 16

RESULT 4

AAW43458 standard; peptide; 16 AA.

AC AAW43458;

DT 08-APR-1998 (first entry)

XX DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).

XX KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
XX KW rheumatoid arthritis; antigen; infectious disease; prophylactic;  
XX KW pristane induced arthritis; PIA.

OS Synthetic.  
 OS Mycobacteria sp.  
 XX  
 PN WO9711966-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 XX  
 PI Elson CJ, Thompson JS;  
 DR WPI; 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAM43451-W4356) which represents  
 the mycobacterial heat shock protein, hsp65 and is designed to study  
 a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAM4948-W4950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 XX  
 SQ Sequence 16 AA;  
 QY  
 DB 6 NVVLEKKMGAPTTND 21  
 1 NVVLEKKMGAPTTND 16  
 Query Match 71.3%; Score 87; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 AAY93330  
 ID AAY93330 standard; peptide; 16 AA.  
 XX  
 AC AAY93330;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of an epitope of heat shock protein 60.  
 XX  
 KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 inflammatory disorder; arthritis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200027870-A1.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 04-NOV-1999; 99WO-IL00595.  
 XX  
 PR 05-NOV-1998; 98US-0107213.  
 XX  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX  
 PI Naparstek Y, Uimansky R, Kaehl Y;

XX  
 DR WPI; 2000-376486/32.  
 XX  
 PT Peptide having a defined sequence is used in vaccines for conferring  
 immunity against autoimmune disease or inflammatory disorders,  
 especially arthritis -  
 XX  
 PS Claim 3; Page 7; 58pp; English.  
 XX  
 CC The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX  
 SQ Sequence 16 AA;  
 QY  
 DB 7 VVLEKKMGAPTTNDG 22  
 1 VVLEKKMGAPTTNDG 16  
 Query Match 71.3%; Score 87; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 AAU99965  
 ID AAU99965 standard; Peptide; 16 AA.  
 XX  
 AC AAU99965;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.  
 XX  
 KW Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 KW autoimmune disease; infectious disease; graft rejection; type I diabetes;  
 KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200248312-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 11-DEC-2001; 2001WO-IL01144.  
 XX  
 PR 11-DEC-2000; 2000IL-0140233.  
 XX  
 PA (PEPT-) PEPTOR LTD.  
 XX  
 PI Elias D, Avron A, Senderowitz H;  
 XX  
 DR WPI; 2002-557613/59.  
 XX  
 PT New backbone cyclized peptide analog of heat shock protein useful in  
 the treatment of e.g. autoimmune disease -  
 XX  
 PS Claim 5; Page 42; 50pp; English.  
 XX  
 CC The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.

```

XX Sequence 16 AA;
SQ Query Match 71.3%; Score 87; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVLEKKGAPITINDG 22
DB 1 VVLEKKGAPITINDG 16

RESULT 7
AAR94779
ID AAR94779 standard; peptide; 15 AA.
AC AAR94779;
XX
XX 11-NOV-1996 (first entry)
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
XX
XX W09610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95MO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides concy. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
XX Sequence 15 AA;
SQ Query Match 68.0%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKWGA 15
DB 1 GPKGRNVVLEKKWGA 15

RESULT 8
AAM43457
ID AAM43457 standard; peptide; 15 AA.
XX

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AC AAM43457;
XX
XX 08-APR-1998 (first entry)
DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).
XX
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
XX rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
XX Synthetic.
XX
XX Mycobacteria sp.
XX
XX W09711966-A1.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96MO-GB02382.
XX
XX 27-SEP-1995; 95GB-0019737.
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX Elson CJ, Thompson JS;
XX
XX WPI; 1997-212851/19.
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
XX for treatment of autoimmune disease esp. arthritis
XX
XX Disclosure; Fig 1a; 91pp; English.
XX
XX This peptide is one of a library (see AAM43451-W4356) which represents
XX the mycobacterial heat shock protein, hsp65 and is designed to study
XX a novel method for the treatment of autoimmune disease e.g. rheumatoid
XX arthritis. This fragment has been allocated as a group 1 peptide which
XX is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
XX hsp65 is known to be an immunodominant antigen in a number of infectious
XX diseases and is linked to pristane induced arthritis (PIA) in vitro,
XX however heat shock proteins and peptides derived from microbial sources
XX may act as self antigens and thus have limited clinical use. The human
XX hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX (see AAM43458-W43950) may be useful in the development of vaccines for
XX prophylaxis or treatment of an autoimmune disease such as rheumatoid
XX arthritis.
XX
XX Sequence 15 AA;
SQ Query Match 68.0%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKWGA 15
DB 1 GPKGRNVVLEKKWGA 15

RESULT 9
AAR94780
ID AAR94780 standard; peptide; 16 AA.
AC AAR94780;
XX
XX 11-NOV-1996 (first entry)
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
XX

```



PN MO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1996-200886/20.  
 XX  
 PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 XX rheumatoid arthritis.  
 XX  
 PS Example 1; Figure 1; 88pp; English.  
 XX  
 CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.  
 CC  
 SQ Sequence 16 AA;  
 XX  
 Query Match 67.2%; Score 82; DB 17; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 NVVLEKKMGAPTTND 21  
 DB 1 NVVLEKKMGAPTTND 16  
 XX  
 RESULT 10  
 AAW43459  
 ID AAW43459 standard; peptide; 15 AA.  
 XX  
 AC AAW43459;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).  
 XX  
 KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KW pristane induced arthritis; PIA.  
 XX  
 OS Synthetic.  
 OS Mycobacteria sp.  
 XX  
 PN MO9711966-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful

PT for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW1948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 57.4%; Score 70; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 KKGAPTTNDG 22  
 DB 1 KKGAPTTNDG 12  
 XX  
 RESULT 11  
 AAR94781  
 ID AAR94781 standard; peptide; 15 AA.  
 XX  
 AC AAR94781;  
 XX  
 DT 11-NOV-1996 (first entry)  
 XX  
 DE Peptide from library spanning whole of hsp65.  
 XX  
 KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KW prophylaxis.  
 XX  
 OS Synthetic.  
 OS  
 PN MO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1996-200886/20.  
 XX  
 PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 XX rheumatoid arthritis.  
 XX  
 PS Example 1; Figure 1; 88pp; English.  
 XX  
 CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune

CC diseases such as rheumatoid arthritis.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 53.3%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00075;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 11 KKWGAPTTNDG 22  
 DB 1 KKWGAPTTNDG 12  
 RESULT 12  
 AAY93331  
 ID AAY93331 standard; peptide; 20 AA.  
 XX  
 AC AAY93331;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of an epitope of heat shock protein 60.  
 XX  
 KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KW inflammatory disorder; arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200027870-A1.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 04-NOV-1999; 99MO-IL00595.  
 XX  
 PR 05-NOV-1998; 98US-0107213.  
 XX  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 PI Naparstek Y, Ulanovsky R, Kaehl Y;  
 PI WPI; 2000-376486/32.  
 XX  
 DR Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -  
 XX  
 PS Claim 4; Page 7; 58pp; English.  
 XX  
 CC The present sequence represents an epitope of the heat shock  
 CC protein 60 (Hsp60) of human origin. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 48.4%; Score 59; DB 21; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 0.011; 3; Indels 0; Gaps 0;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 VLEKKWGAPTTNDG 22  
 DB 2 VLEKKWGAPTTNDG 17  
 RESULT 13  
 AAU99966  
 ID AAU99966 standard; peptide; 20 AA.  
 XX  
 AC AAU99966;  
 XX  
 DT 07-OCT-2002 (first entry)

XX  
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #3.  
 XX  
 KW Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 KW autoimmune disease; infectious disease; graft rejection; type I diabetes;  
 KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 KW arteriosclerosis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN MO200248312-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 11-DEC-2001; 2001MO-IL01144.  
 XX  
 PR 11-DEC-2000; 2000IL-0140233.  
 XX  
 PA (PEPT-) PEPTOR LTD.  
 XX  
 PI Elias D, Avron A, Senderowitz H;  
 PI WPI; 2002-557613/59.  
 XX  
 DR New backbone cyclized peptide analog of heat shock protein useful in  
 XX the treatment of e.g. autoimmune disease -  
 XX  
 PT Claim 5; Page 42; 50pp; English.  
 XX  
 PS The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 48.4%; Score 59; DB 23; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 0.011; 3; Indels 0; Gaps 0;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 VLEKKWGAPTTNDG 22  
 DB 2 VLEKKWGAPTTNDG 17  
 RESULT 14  
 AAR94778  
 ID AAR94778 standard; peptide; 16 AA.  
 XX  
 AC AAR94778;  
 XX  
 DT 11-NOV-1996 (first entry)  
 XX  
 DE Peptide from library spanning whole of hsp65.  
 XX  
 KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KW prophylaxis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95MO-GB02295.  
 XX

```

PR 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
DR
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
XX Sequence 16 AA;
SQ
Query Match 46.7%; Score 57; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEK 11
DB 6 GPKGRNVVLEK 16
RESULT 15
AAM43456
ID AAM43456 standard; peptide; 16 AA.
XX
XX AAM43456;
AC
XX
XX 08-APR-1998 (first entry)
DT
XX
XX Mycobacteria sp. hsp68 derived peptide (group 1 #6).
DE
XX
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
KM pristane induced arthritis; PIA.
XX
XX Synthetic.
OS Mycobacteria sp.
OS
XX
XX WO9711966-A1.
PN
XX
XX 03-APR-1997.
PD
XX
XX 26-SEP-1996; 96WO-GB02382.
PF
XX
XX 27-SEP-1995; 95GB-0019737.
PR
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
PA
XX
XX Elson CJ, Thompson JS;
PI
XX
XX WPI; 1997-212851/19.
DR
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
PT
XX
XX Disclosure; Fig 1a; 91pp; English.
PS
XX
XX This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study

```

```

CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro.
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM1948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
XX Sequence 16 AA;
SQ
Query Match 46.7%; Score 57; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEK 11
DB 6 GPKGRNVVLEK 16

```

Search completed: December 30, 2003, 16:23:46  
Job time : 42 secs



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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:01 ; Search time 31 Seconds

(without alignments)  
141.238 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 160453

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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9	35	28.7	20	10	US-09-847-761-44019
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12	34	27.9	14	12	US-10-323-046-12
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15	34	27.9	14	15	US-10-106-804B-10

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18	34	27.9	17	12	US-10-395-032-50	Sequence 50, Appl
19	34	27.9	17	15	US-10-006-869-50	Sequence 50, Appl
20	34	27.9	17	15	US-10-193-653-68	Sequence 68, Appl
21	34	27.9	22	15	US-10-106-804B-20	Sequence 20, Appl
22	33	27.0	20	12	US-10-280-066-439	Sequence 439, Appl
23	32	26.2	9	12	US-10-228-167A-3	Sequence 3, Appl1
24	32	26.2	12	11	US-09-753-126-100	Sequence 100, Appl
25	32	26.2	12	11	US-09-896-896A-64	Sequence 64, Appl
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27	32	26.2	20	9	US-09-841-132-228	Sequence 228, Appl
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30	31.5	25.8	16	10	US-09-995-587A-34	Sequence 34, Appl
31	31.5	25.8	16	10	US-09-995-587A-35	Sequence 35, Appl
32	31.5	25.8	17	10	US-09-995-587A-36	Sequence 36, Appl
33	31.5	25.8	17	15	US-10-128-449A-16	Sequence 16, Appl
34	31	25.4	13	11	US-09-852-455-68	Sequence 68, Appl
35	31	25.4	15	12	US-10-350-405-5	Sequence 5, Appl
36	31	25.4	15	12	US-10-350-405-5	Sequence 5, Appl
37	31	25.4	15	15	US-10-121-746-70	Sequence 70, Appl
38	31	25.4	18	11	US-09-828-000-6	Sequence 6, Appl1
39	31	25.4	18	12	US-10-269-806-23	Sequence 23, Appl
40	31	25.4	18	12	US-10-269-806-156	Sequence 156, Appl
41	31	25.4	18	12	US-10-405-588-6	Sequence 6, Appl1
42	31	25.4	19	11	US-09-764-872-322	Sequence 322, Appl
43	30	24.6	14	10	US-09-805-301-80	Sequence 80, Appl
44	30	24.6	16	12	US-10-161-791-228	Sequence 228, Appl
45	30	24.6	18	12	US-10-125-669A-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
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Sequence 1, Application US/09847637B  
Patent No. US20020150586A1  
GENERAL INFORMATION:  
APPLICANT: Naparstek, Yaakov  
APPLICANT: Umanetsky, Rina  
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF  
FILE REFERENCE: 13125-002001  
CURRENT APPLICATION NUMBER: US/09/847,637B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: PCT/IL99/00595  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,213  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-847-637B-1  
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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US-09-847-637B-2  
Sequence 2, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Ulanesky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-2

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Best Local Similarity 100.0%; Pred. No. 2,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GPKGRNVLEKKGAP 16

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; Sequence 3, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Ulanesky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-3

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Best Local Similarity 100.0%; Pred. No. 7,9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Ulanesky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-637B-4

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DB 2 VLEKKGAPITNDG 17

RESULT 5
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; Sequence 44019, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:22:55 ; Search time 22 Seconds

(Without alignments)  
42,311 Million cell updates/sec

Title: US-09-847-637B-1

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Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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US-08-467-822-11  
Sequence 11, Application US/08467822  
Patent No. 5843460  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,822  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-467-822-11

Query Match 29.5%; Score 36; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 2.5e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GPGKRVN 8

RESULT 2  
US-08-432-697-11  
Sequence 11, Application US/08432697  
Patent No. 6248330  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-432-697-11

Query Match 29.5%; Score 36; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 2.5e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGKRVN 7  
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DB 2 GPGKRVN 8

RESULT 3  
US-08-466-248-11  
Sequence 11, Application US/08466248

Patent No. 6258359

GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-248-11

Query Match 29.5%; Score 36; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 2.5e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGKRVN 7  
||:||||  
DB 2 GPGKRVN 8

RESULT 4  
US-08-204-487-4  
Sequence 4, Application US/08204487  
Patent No. 5565425  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, NAOKI  
APPLICANT: NAKASHIMA, HIDEKI  
APPLICANT: MOSUCHI, WATARU  
APPLICANT: TANAKA, SHIGEKI  
APPLICANT: DOSAKO, SHUN'ICHI  
APPLICANT: KAWASAKI, YOSHIHIRO  
APPLICANT: UCHIDA, TOSHIKI



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# OM protein - protein search, using sw model

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(without alignments)  
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Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 76: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	28.9	14	2	154945	gene C protein - B
2	26	28.9	16	2	E58501	25K kidney and gal
3	25	27.8	13	1	MTCMAD	melanotropin alpha
4	25	27.8	13	1	MTROAD	melanotropin alpha
5	24	26.7	15	2	JN0730	hypothetical 1.7K
6	23	25.6	11	2	A34243	H-hyosoporphin - Ja
7	23	25.6	15	2	PH0760	T-cell receptor be
8	22	24.4	8	2	A31570	angiotensin-conver
9	21	23.3	11	2	VHRT	morphogenetic neur
10	21	23.3	11	2	VHNU	morphogenetic neur
11	21	23.3	11	2	VHBO	morphogenetic neur
12	21	23.3	11	2	VHXA	morphogenetic neur
13	21	23.3	11	2	VHFX	morphogenetic neur
14	21	23.3	12	2	S65730	hemoglobin, extrac
15	21	23.3	12	2	I46922	gene beta protein
16	21	23.3	13	2	A32734	enkephalin precurs
17	21	23.3	13	2	IS0173	alpha-2 collagen -
18	21	23.3	13	2	A86126	hypothetical prote
19	21	23.3	13	2	S01904	H+-transporting tw
20	21	23.3	14	2	S23376	collagen alpha cha
21	21	23.3	16	2	PH0748	T-cell receptor be
22	20	22.2	10	2	B33710	ornithine decarbox
23	20	22.2	10	2	A55695	proteoglycan core
24	20	22.2	12	2	S65629	protoporphyrinogen
25	20	22.2	13	2	S04013	lignin peroxidase
26	20	22.2	13	2	PH0928	T-cell receptor be
27	20	22.2	14	2	S13864	methyl coenzyme M
28	20	22.2	14	2	A59018	MUC1 enhancer bind
29	20	22.2	15	2	T46625	hypothetical prote

30	20	22.2	15	2	D28587	T-cell receptor be
31	20	22.2	16	1	MTDFBS	melanotropin beta
32	20	22.2	16	2	G45681	orf 61.1 - phage T
33	20	22.2	16	2	S36876	aquacobalamn redu
34	19	21.1	11	2	A34662	Achataia cardio-ex
35	19	21.1	11	2	D56979	collagen alpha 1(I
36	19	21.1	13	2	T08533	hypothetical prote
37	19	21.1	13	2	S22995	hypothetical prote
38	19	21.1	13	2	S13273	polyisialoglycoprot
39	19	21.1	13	2	S57567	T cell receptor V-
40	19	21.1	13	2	G83988	hypothetical prote
41	19	21.1	15	2	S21241	oligo-1,6-glucosid
42	19	21.1	15	2	PA0102	fructose-bisphosph
43	19	21.1	16	2	B28587	T-cell receptor be
44	19	21.1	16	2	F53284	T-cell receptor be
45	19	21.1	16	2	PH0767	T-cell receptor be

## ALIGNMENTS

RESULT 1  
154945  
gene C protein - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999  
C/Accession: 154945  
R/Tao, T.; Bourne, J.C.; Blumenthal, R.M.  
J. Bacteriol. 173, 1367-1375, 1991  
A/Title: A family of regulatory genes associated with type II restriction-modification  
A/Reference number: 154945; MUID:91139577; PMID:199588  
A/Accession: 154945  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-14 <RES>  
A/Cross-references: GB:M63619; NID:G147664; PIDN:AA24555.1; PID:G147665

Query Match 28.9%; Score 26; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 6.7e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RNVLEKK 12  
DB 2 KEVIMKK 9

RESULT 2  
B58501  
25k kidney and gallbladder stone protein - unidentified bacterium (fragment)  
C/Species: unidentified bacterium  
C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C/Accession: B58501  
R/Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A/Description: The proteins of kidney and gallbladder stones.  
A/Reference number: A58501  
A/Accession: B58501  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <BIN>  
A/Experimental source: human kidney and gallbladder stones  
A/Note: tentative identification of 8-Gly and 13-Ser

Query Match 28.9%; Score 26; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 7.7e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KGRNVLEKK 12  
DB 6 KGRNVLSKE 15

RESULT 3

## MTCMD

melanotropin alpha - Arabian camel

C/Species: Camelus dromedarius (Arabian camel)

C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C/Accession: A01464

R/Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.

Biochemistry 14, 947-952, 1975

A/Title: Isolation, characterization, and amino acid sequence of melanotropins from camel

A/Reference number: A90393; PMID:75146434; PMID:1125179

A/Accession: A01464

A/Molecule type: protein

A/Residues: 1-13 &lt;LTC&gt;

C/Superfamily: corticotropin-lipotropin

C/Keywords: acetylated amino end; blocked carboxyl end; hormone; pituitary

F/1/Modified site: acetylated amino end (Ser) (partial) #status experimental

F/13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 9.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KMGAP 16  
DB 8 RMGKP 12

## RESULT 4

MTHOAD

melanotropin alpha - horse

C/Species: Equus caballus (domestic horse)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C/Accession: A91785; A01464

R/Dixon, J.S.; Li, C.H.

J. Am. Chem. Soc. 82, 4568-4572, 1960

A/Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse

A/Reference number: A91785

A/Accession: A91785

A/Molecule type: protein

A/Residues: 1-13 &lt;DIK&gt;

C/Superfamily: corticotropin-lipotropin

C/Keywords: blocked amino end; blocked carboxyl end; hormone; pituitary

F/1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

F/13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 9.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KMGAP 16  
DB 8 RMGKP 12

## RESULT 5

JN0730

hypothetical 1.7K protein - phage SPPI

N/Alternate names: hypothetical protein 42.1

C/Species: phage SPPI

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999

C/Accession: JN0730

R/Chai, S.; Stepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.

Gene 129, 41-49, 1993

A/Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPPI 9

A/Reference number: JN0729; PMID:93328123; PMID:8335255

A/Accession: JN0730

A/Molecule type: DNA

A/Residues: 1-15 &lt;CHA&gt;

A/Cross-references: EMBL:X65941

Query Match 26.7%; Score 24; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. No. 1.6e+03;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPKGRNVVL 9

DB 5 GPPFRSMVL 13

## RESULT 6

A34243

H-hydrophorin - Japanese flounder (fragment)

C/Species: Paralichthys olivaceus (Japanese flounder)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 12-Feb-1999

C/Accession: A34243

R/Seko, A.; Kikajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.

J. Biol. Chem. 264, 15922-15929, 1989

A/Title: Structural studies of fertilization-associated carbohydrate-rich glycoprotein

of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide w

A/Reference number: A34243; PMID:89380184; PMID:2777771

A/Accession: A34243

A/Molecule type: protein

A/Residues: 1-11 &lt;SEK&gt;

A/Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 25.6%; Score 23; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGRNVVL 10  
DB 2 GSVGAGNVTL 11

## RESULT 7

PH0760

T-cell receptor beta chain (H2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C/Accession: PH0760

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; PMID:9207846; PMID:1836010

A/Accession: PH0760

A/Molecule type: mRNA

A/Residues: 1-15 &lt;CAB&gt;

A/Cross-references: EMBL:X60855; NID:951194; PIDN:CAA43245.1; PID:951195

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match 25.6%; Score 23; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 2.3e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKGRN 6  
DB 5 PTKRN 9

## RESULT 8

A31570

angiotensin-converting enzyme inhibitor - yellowfin tuna

C/Species: Thunnus albacares (yellowfin tuna)

C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000

C/Accession: A31570

R/Kobama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A/Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A/Reference number: A31570; PMID:88326322; PMID:3415688

A/Accession: A31570

A/Molecule type: protein

A/Residues: 1-8 &lt;KOH&gt;

A/Note: The source is designated as Neothunnus macropterus

C/Superfamily: unassigned animal peptides

C/Keywords: angiotensin-converting enzyme inhibitor

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:26:11 ; Search time 10 Seconds  
(without alignments)  
75.243 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVYLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 872

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	27.8	13	MLA_ANOCA	P41589 anolis caro
2	25	27.8	13	MLA_CAMDR	P01198 camelus dro
3	22	24.4	8	ACT_THUL	P18691 chunnus alb
4	21	22.3	11	MORN_HUMAN	P01163 homo saplen
5	20	22.2	13	LIGA_TRAVS	P20011 tremeles ve
6	20	22.2	14	MGRX_METTM	P58815 methanobact
7	20	22.2	16	MLB_SQUAC	P01207 equalus aca
8	19	21.1	9	TKEL_LOCM1	P16223 locusta mig
9	19	21.1	11	CEPI_ACHFU	P22790 achnatna fu
10	19	21.1	12	UP01_CABEL	P55954 caenothabdi
11	19	21.1	13	IDHP_RAT	P56574 rattus norv
12	19	21.1	15	UC06_MAIZE	P80612 zea mays (m
13	19	21.1	16	NMPX_SOLUT	P80501 solanum tub
14	18	20.0	9	CONO_CONGR	P05486 conus geogr
15	18	20.0	10	BPP8_BOTIN	P30426 bochrops in
16	18	20.0	12	BPP_VIPAS	P31351 vipera aspi
17	18	20.0	10	PSB3_PHYPA	P80662 physcomitre
18	18	20.0	12	RFL_CONSP	P58805 conus spuri
19	18	20.0	13	PSB7_PINPS	P18668 pinus pinas
20	18	20.0	14	TAT_HVIW2	P15052 human immun
21	18	20.0	15	TAT_HVI18	P80072 bacillus th
22	18	20.0	15	MLAT_BACTO	P30425 bochrops in
23	17.5	19.4	5	BPP7_BOTIN	P13737 mytilus edu
24	17	18.9	6	CTP2_MYTED	P41491 locusta mig
25	17	18.9	6	LOK1_LOCM1	P21140 leucophaea
26	17	18.9	8	LOK1_LEUMA	P21141 leucophaea
27	17	18.9	8	LOK2_LEUMA	P21142 leucophaea
28	17	18.9	8	LOK3_LEUMA	P21143 leucophaea
29	17	18.9	8	LOK4_LEUMA	P19987 leucophaea
30	17	18.9	8	LOK5_LEUMA	P19988 leucophaea
31	17	18.9	8	LOK6_LEUMA	P19989 leucophaea
32	17	18.9	8	LOK7_LEUMA	P19990 leucophaea
33	17	18.9	8	LOK8_LEUMA	

34	17	18.9	8	1	RTJ3_BOVIN	P82929 bos taurus
35	17	18.9	9	1	FAR6_MACRS	P83279 macrobrachi
36	17	18.9	9	1	SAP_STOVA	P24047 stomopneute
37	17	18.9	10	1	FAR6_PANRE	P82660 panagrellus
38	17	18.9	10	1	HTF1_ROMMI	P18110 romalea mic
39	17	18.9	10	1	HTF2_CARMO	P1385 carastus m
40	17	18.9	10	1	HTF_HELZE	P16353 heliothis z
41	17	18.9	10	1	HTF_NAUCI	P10939 nauphoeta c
42	17	18.9	10	1	HTF_TABAT	P14596 tabanus atr
43	17	18.9	10	1	LABA_JATMU	P13270 jatropna mu
44	17	18.9	10	1	TPIS_NICPL	P19118 nicotiana p
45	17	18.9	12	1	H2AX_ONCMY	P83327 oncorhynch

#### ALIGNMENTS

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RESULT 1
MLA_ANOCA          STANDARD;          PRT;          13 AA.
AC P41589;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Anolis carolinensis (Green anole) (American chameleon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_Taxid=28377;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary; PubMed=167689;
RX MEDLINE=92270473;
RA Dore R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT "Detection of a novel sequence change in the major form of alpha-MSH
RT isolated from the intermediate pituitary of the reptile, Anolis
RT carolinensis."
RL Peptides 12:1261-1266(1991).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR InterPro: IPR001941; Mcoortn ACTH.
DR Pfam: PF00976; ACTH_domain; I.
KW Hormone; Amidation.
FT MOD_RES 13
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1608 MW; PP990A7358B09C1 CRC64;

Query Match          27.8%; Score 25; DB 1; Length 13;
Beet Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KWGAP 16
DB 8 RWGKP 12

RESULT 2
MLA_CAMDR          STANDARD;          PRT;          13 AA.
AC P01198;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_Taxid=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C.dromedarius;
RX MEDLINE=7514634; PubMed=1125179;
RA Li C.H., Danto W.O., Chung D., Rao A.J.;
RA "Isolation, characterization, and amino acid sequence of

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RT melanotropine from camel pituitary glands."
RL Biochemistry 14:947-952(1975).
RN [2]
RC SPECIES=Horse; TISSUE=Pituitary;
RA Dixon J.S., Li C.H.;
RT "The isolation and structure of alpha-melanocyte-stimulating hormone
from horse pituitaries."
RL J. Am. Chem. Soc. 82:4568-4572(1960).
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; A01464; MTCMAD.
DR PIR; A91785; MTHOAD.
DR InterPro; IPR001941; Mcoctin_ACTH.
DR Pfam; PF00976; ACTH_domain; 1.
KW Hormone; Acetylation; Amidation.
FT MOD_RES 1 ACETYLATION (IN ABOUT 50% OF CAMEL
FT SEQUENCE 1 MOLECULES).
SQ MOD_RES 13 13 AMIDATION.
Query Match 27.8%; Score 25; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KWGAP 16
DB 8 RWGAP 12

RESULT 3
ACI THUAL STANDARD; PRT; 8 AA.
ID ACI THUAL
AC P18691;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunus albacares (Yellowfin tuna) (Neochunus macropterus).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle."
RT Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051P1B7 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 KWG 14
DB 5 KWG 7

RESULT 4
MORN HUMAN STANDARD; PRT; 11 AA.
ID MORN HUMAN
AC F01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),

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OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RA MEDLINE=82035850; PubMed=7290191;
RX Bodemuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
from coelenterates to humans."
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegans, and H.attenuata;
RA Schaller H.C., Bodemuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
hydra."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Bitt C., Zachmann B., Bodemuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra."
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH45-CA2 cells
in the G2/mitosis transition."
RL EMBO J. 8:3311-3318(1989).
CC -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
IN THE G2/MITOSIS TRANSITION.
CC CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
BEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
CC PIR; A01427; YHRT.
DR PIR; A93960; YHXA.
DR PIR; B01427; YHHD.
DR PIR; B93900; YHUPHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 23.3%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKGNVVL 9
DB 3 FGSKVIL 10

RESULT 5
LIGA TRAVE STANDARD; PRT; 13 AA.
ID LIGA TRAVE
AC P20011;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ligninase A (EC 1.11.1.14) (Diatrypropene peroxidase) (Lignin
peroxidase) (Fragment).
OS Trameetes vericolor (White-rot fungus).
OC Bkaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trameetes.
OX NCBI_TaxID=5325;
RN [1]

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:41 ; Search time 28 Seconds

(without alignments)  
147,459 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4022

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_ivirus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	28.9	14	2	Q47599	Q47599 escherichia
2	25	27.8	10	11	O70580	O70580 mus musculus
3	24	26.7	10	4	O9UNF2	O9UNF2 homo sapien
4	24	26.7	15	2	O9RAP5	O9RAP5 brevidinon
5	23	25.6	11	15	O83410	O83410 mouse mamma
6	23	25.6	13	15	O85645	O85645 mouse mamma
7	23	25.6	16	4	O9UC18	O9UC18 homo sapien
8	23	25.6	16	8	O9T2V8	O9T2V8 homo sapien
9	23	25.6	16	10	O9S8D6	O9S8D6 triticum ae
10	22	24.4	14	10	O9RS17	O9RS17 escherichia
11	22	24.4	14	10	P82322	P82322 pisum sativ
12	21.5	23.9	13	5	O9WS06	O9WS06 drosophila
13	21	23.3	8	8	O94PX5	O94PX5 felis silve
14	21	23.3	8	8	O94VB2	O94VB2 varanus sal
15	21	23.3	8	8	O94PX7	O94PX7 felis silve
16	21	23.3	8	8	O94PX6	O94PX6 felis libyc

17	21	23.3	8	8	Q94VA7	Q94VA7 varanus sal
18	21	23.3	8	8	Q94VB5	Q94VB5 varanus sal
19	21	23.3	9	8	Q94VC6	Q94VC6 varanus pil
20	21	23.3	10	8	Q94VD5	Q94VD5 varanus pil
21	21	23.3	12	7	O31006	O31006 bos taurus
22	21	23.3	13	7	O9TNO8	O9TNO8 homo sapien
23	21	23.3	13	8	O9MOK0	O9MOK0 cervus elap
24	21	23.3	13	8	O9MOK6	O9MOK6 rupicapra r
25	21	23.3	13	8	O9MOK3	O9MOK3 capra ibex
26	21	23.3	13	16	O8X4F5	O8X4F5 escherichia
27	21	23.3	15	4	O9BXX4	O9BXX4 homo sapien
28	21	23.3	15	4	O00604	O00604 homo sapien
29	21	23.3	15	8	P92076	P92076 euhadra her
30	21	23.3	16	5	O9TWS8	O9TWS8 lamellibrac
31	21	23.3	16	5	O9TFJ0	O9TFJ0 trypanosoma
32	20	22.2	8	4	O16468	O16468 homo sapien
33	20	22.2	10	2	O9R7J8	O9R7J8 helicobacte
34	20	22.2	10	11	O63389	O63389 rattus norv
35	20	22.2	11	2	O9EUB3	O9EUB3 escherichia
36	20	22.2	11	15	O9ADI8	O9ADI8 human immun
37	20	22.2	12	4	O9UHQ9	O9UHQ9 homo sapien
38	20	22.2	12	4	O9H4X3	O9H4X3 homo sapien
39	20	22.2	12	15	O8ODY5	O8ODY5 human immun
40	20	22.2	12	15	O8ODY4	O8ODY4 human immun
41	20	22.2	12	15	O8ODY4	O8ODY4 human immun
42	20	22.2	12	15	O8ODY4	O8ODY4 human immun
43	20	22.2	12	15	O8ODY4	O8ODY4 human immun
44	20	22.2	12	15	O8ODY4	O8ODY4 human immun
45	20	22.2	12	15	O8ODY6	O8ODY6 human immun

## ALIGNMENTS

## RESULT 1

Q47599 PRELIMINARY; PRT; 14 AA.  
ID Q47599  
AC Q47599;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE C (Fragment).  
GN C.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP MEDLINE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
modification systems".  
RL J. Bacteriol. 173:1367-1375 (1991).  
DR EMBL; M63619; AAA2455.1; -.  
FT NON TER  
SQ SEQUENCE 14 AA; 1705 MW; 77B6CAG0581A4F3B CRC64;

Query Match 28.9%; Score 26; DB 2; Length 14;  
Best local similarity 50.0%; Pred. NO. 1.5e+03;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RNVLEKK 12  
Db :||:||||  
2 KEVIMKK 9

## RESULT 2

O70580 PRELIMINARY; PRT; 10 AA.  
ID O70580  
AC O70580;  
DT 01-AUG-1998 (TRENBLREL. 07, Created)  
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Carbonic anhydrase III (Fragment).  
 GN CAR3 OR CAR3 OR CA3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sowden J., Smith H., Morrison K., Edwards Y.;  
 RT "Sequence comparisons and functional studies of the proximal promoter  
 of the carbonic anhydrase 3 (CA3) gene.";  
 RL Gene 214:157-165(1999).  
 DR EMBL; AJ006474; CAA07057.1; -.  
 DR MGD; MGI:88270; Car3.  
 DR MGD; MGI:1351477; Car3.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1105 MW; 567FE71ADC37B13 CRC64;

Query Match 26.7%; Score 25; DB 11; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 LEKKGAP 16  
 DB 1 MAKEWATP 8

RESULT 3  
 Q9UNF2 PRELIMINARY; PRT; 10 AA.  
 AC Q9UNF2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)  
 DE 01-MAY-2000 (TrEMBLrel. 13, last annotation update)  
 GN Alpha 1 collagen (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteheria; Primates; Carnivora; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ratcliffe T.A., Vitz J.R., Ray D.B.;  
 RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene  
 at 10,828 bp: cytosine replaces adenine.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF128441; AAD32608.1; -.  
 KW Collagen.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 26.7%; Score 24; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKG 4  
 DB 4 GPKG 7

RESULT 4  
 Q9R4P5 PRELIMINARY; PRT; 15 AA.  
 AC Q9R4P5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, last annotation update)  
 DE Ribosomal protein L24 (Fragment).  
 OS Brevundimonas diminuta (Pseudomonas diminuta).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Brevundimonas.  
 OX NCBI\_TaxID=293;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95244309; PubMed=7727274;  
 RA Ochi K.;  
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically  
 RT defined genus, Pseudomonas, and its relatives.";  
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).  
 SQ SEQUENCE 15 AA; 1513 MW; 8BA258CFA725914F CRC64;

Query Match 26.7%; Score 24; DB 2; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 3.5e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KGRNVVL 9  
 DB 6 KGRNVVL 12

RESULT 5  
 O83410 PRELIMINARY; PRT; 11 AA.  
 AC O83410;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
 DE Superantigen (Fragment).  
 GN SAG.  
 OS Mouse mammary tumor virus.  
 OC Viruses; Retrovirdae; Betaretrovirus.  
 OX NCBI\_TaxID=11757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mtv-6;  
 RX MEDLINE=95133174; PubMed=7831795;  
 RA Cho K., Ferrick D.A., Morris D.W.;  
 RT "Structure and biological activity of the subgenomic Mtv-6 endogenous  
 RT provirus.";  
 RL Virology 206:395-402(1995).  
 DR EMBL; L37518; AAA66963.1; -.  
 DR InterPro; IPR001213; MMTV\_SAG.  
 DR Pfam; PF01054; MMTV\_SAG; 1.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1401 MW; 5B6B080A7326C6D7 CRC64;

Query Match 25.6%; Score 23; DB 15; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 LEKKM 13  
 DB 4 LEKKM 8

RESULT 6  
 O85645 PRELIMINARY; PRT; 13 AA.  
 AC O85645;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
 DE Endogenous mouse mammary tumor proviral LTR gene product, 5' end  
 DE (Fragment).  
 OS Mouse mammary tumor virus.  
 OC Viruses; Retrovirdae; Betaretrovirus.  
 OX NCBI\_TaxID=11757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83138005; PubMed=6298469;  
 RA Wheeler D.A., Butel J.S., Medina D., Cardiff R.D., Hager G.L.;  
 RT "Transcription of mouse mammary tumor virus: Identification of a  
 RT candidate mRNA for the long terminal repeat gene product.";

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:36 ; Search time 35 Seconds

(without alignments)  
72.561 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90  
Sequence: 1 GPKGRNVVLEKMKCAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 360314

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_19Jun03:.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	100.0	16	21	AAV93329	Amino acid sequence
2	90	100.0	16	23	AAU99964	Mycobacterium tube
3	83	92.2	15	17	AAK94779	Peptide from libra
4	83	92.2	15	18	AAW43457	Mycobacteriella sp. h
5	61	67.8	16	17	AAK94780	Peptide from libra
6	61	67.8	16	18	AAW43458	Mycobacteriella sp. h
7	57	63.3	16	17	AAK94778	Peptide from libra
8	57	63.3	16	18	AAW43456	Mycobacteriella sp. h
9	55	61.1	16	21	AAV93330	Amino acid sequence

10	55	61.1	16	23	AAU99965	Mycobacterium tube
11	47	52.2	11	22	AAK88272	Hsp-65 peptide epi
12	43	47.8	10	22	AAK88269	Hsp-65 peptide epi
13	39	43.3	9	22	AAK88279	Peptide from libra
14	38	42.2	15	17	AAK94781	Peptide from libra
15	38	42.2	15	18	AAW43459	Mycobacteriella sp. h
16	34	37.8	14	21	AAK10751	Fibrin gel binding
17	34	37.8	14	21	AAK01586	Proteoglycan bindi
18	34	37.8	14	22	AAK35931	NCAW/heparin bindi
19	34	37.8	14	23	AAU85712	Neural cell adhesi
20	34	37.8	14	23	AAU50288	Cytochrome b12 N-t
21	34	37.8	15	22	AAK64099	G. multiflorum rec
22	32	35.6	16	22	ABG71559	Melanocyte stimula
23	31	34.4	12	22	AAK90858	Tie-1 binding surr
24	31	34.4	13	23	AAK48084	Human secreted pro
25	30	33.3	10	21	AAK32456	Delivery peptide u
26	30	33.3	14	18	AAK38766	Nucleic acid (NA)
27	30	33.3	14	18	AAW24451	Gb2 N-terminal SH
28	30	33.3	15	18	AAK25443	Hepatitis C virus
29	29.5	32.8	15	19	AAK37382	G protein-coupled
30	29.5	32.8	16	24	ABK62686	Molt-4 leukaemia c
31	29	32.2	7	23	ABJ04516	Human tumor-associ
32	29	32.2	9	22	AAK45892	Nuclear localisati
33	29	32.2	13	17	AAK69652	Compressing peptid
34	29	32.2	13	18	AAK19794	Human procathepsin
35	29	32.2	13	23	ABK97728	Human procathepsin
36	29	32.2	13	23	ABK97729	Human procathepsin
37	29	32.2	14	22	AAK97155	Human procathepsin
38	29	32.2	14	22	AAK00717	Human procathepsin
39	29	32.2	14	23	ABK66058	Human procathepsin
40	29	32.2	15	19	AAK75543	Collagen II specif
41	29	32.2	15	23	ABK61615	Human DPER-3 pepti
42	28.5	31.7	10	22	AAK48442	Human complementar
43	28	31.1	9	19	AAK56753	A. tumefaciens ant
44	28	31.1	9	22	AAU02332	HIV binding TADG-1
45	28	31.1	12	18	AAK38002	NW domain binding

#### ALIGNMENTS

AAV93329	AAV93329 standard; peptide, 16 AA.
XX	AAV93329;
XX	04-SEP-2000 (first entry)
DT	Amino acid sequence of an epitope of heat shock protein 60.
DE	Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW	inflammatory disorder; arthritis.
XX	
OS	Mycobacterium tuberculosis.
XX	WO200027870-A1.
PN	18-MAY-2000.
PD	
XX	04-NOV-1999; 99WO-IL00595.
PF	
XX	05-NOV-1998; 98US-0107213.
PR	
XX	(HADA-) HADA/IT MEDICAL RES SERVICES & DEV.
PA	Naparetek Y, Ulimansky R, Kaeshi Y;
XX	WPI; 2000-376486/32.
XX	Peptide having a defined sequence is used in vaccines for conferring
PT	immunity against autoimmune disease or inflammatory disorders,
PT	especially arthritis -

```

XX PS Claim 2, Page 7, 58pp; English.
XX CC
XX CC The present sequence represents an epitope of the heat shock protein
XX CC 60 (hsp60) of Mycobacterium tuberculosis. The peptide, and the
XX CC nucleic acid encoding it, are useful in vaccines for conferring
XX CC immunity against autoimmune disease or inflammatory disorders,
XX CC especially arthritis. The peptide may also be used to raise
XX CC antibodies, which are then used for passive immunisation.
XX SQ
XX Sequence 16 AA;
XX
XX Query Match 100.0%; Score 90; DB 21; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-08;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Db 1 GPKGRNVLEKKWGAP 16
XX
XX RESULT 2
XX AAU99964 standard; Peptide; 16 AA.
XX
XX AC AAU99964;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.
XX
XX KW Heat shock protein; hsp; hsp60; chronic inflammatory disease;
XX KW autoimmune disease; infectious disease; graft rejection; type 1 diabetes;
XX KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
XX KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
XX KW arteriosclerosis.
XX
XX OS Mycobacterium tuberculosis.
XX
XX PN WO200248312-A2.
XX
XX PD 20-JUN-2002.
XX
XX PF 11-DEC-2001; 2001WO-1101144.
XX
XX PR 11-DEC-2000; 2000IL-0140233.
XX
XX PA (PEPT-) PEPTOR LTD.
XX
XX PI Elias D, Avron A, Senderowitz H;
XX
XX DR WPI; 2002-557613/59.
XX
XX PT New backbone cyclised peptide analog of heat shock protein useful in
XX PT the treatment of e.g. autoimmune disease -
XX
XX PS Claim 5; Page 42; 50pp; English.
XX
XX CC The invention relates to backbone cyclised peptide analogues or
XX CC antagonists of heat shock protein (hsp). The analogues and antagonists
XX CC are useful in the treatment of chronic inflammatory disease, autoimmune
XX CC disease, infectious disease and graft rejection, and for diagnosing
XX CC autoimmune and inflammatory disease including juvenile rheumatoid
XX CC arthritis, type 1 diabetes, multiple sclerosis, systemic lupus
XX CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
XX CC arteriosclerosis. This sequence represents a backbone cyclised peptide
XX CC analogue of a heat shock protein.
XX SQ
XX Sequence 16 AA;
XX
XX Query Match 100.0%; Score 90; DB 23; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-08;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX QY 1 GPKGRNVLEKKWGAP 16
XX DB 1 GPKGRNVLEKKWGAP 16
XX
XX RESULT 3
XX AAR94779 standard; peptide; 15 AA.
XX
XX AC AAR94779;
XX
XX DT 11-NOV-1996 (first entry)
XX
XX DE Peptide from library spanning whole of hsp65.
XX
XX KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX KW prophylaxis.
XX
XX OS Synthetic.
XX
XX PN WO9610039-A1.
XX
XX PD 04-APR-1996.
XX
XX PF 27-SEP-1995; 95WO-GB02295.
XX
XX PR 27-SEP-1994; 94GB-0019553.
XX
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX PI Elson CJ, Thompson SJ;
XX
XX DR WPI; 1996-200888/20.
XX
XX PT Polypeptide derived from bacterial heat shock protein 65 - for use
XX PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX PT rheumatoid arthritis.
XX
XX PS Example 1; Figure 1; 88pp; English.
XX
XX CC AAR94773-R94878 are overlapping peptides of a library spanning the
XX CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX CC prepared from the library and used to immunise mice, after 10 days the
XX CC mice received injections of pristane to induce arthritis and the
XX CC animals examined for incidence of arthritis. A preferred anti-arthritis
XX CC peptide was found to correspond to residues 21-31 of full length hsp65
XX CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX CC diseases such as rheumatoid arthritis.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 92.2%; Score 83; DB 17; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GPKGRNVLEKKWGA 15
XX DB 1 GPKGRNVLEKKWGA 15
XX
XX RESULT 4
XX AAM43457 standard; peptide; 15 AA.
XX
XX ID AAM43457
XX
XX AC AAM43457;
XX
XX DT 08-APR-1998 (first entry)
XX
XX DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).
XX

```



KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.  
 OS Synthetic.  
 OS Mycobacteria sp.  
 PN WO9711966-A1.  
 XX  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 PI Elson CJ, Thompson JS;  
 XX  
 DR WPI, 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW43458-W43950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 CC  
 SQ Sequence 15 AA;  
 Query Match 92.2%; Score 83; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKWGA 15  
 |||||  
 DB 1 GPKGRNVLEKKWGA 15  
 |||||  
 RESULT 5  
 AAR94780  
 ID AAR94780 standard; peptide; 16 AA.  
 XX  
 AC AAR94780;  
 XX  
 DT 11-NOV-1996 (first entry)  
 XX  
 DE Peptide from library spanning whole of hsp65.  
 XX  
 KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM prophylaxis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX

PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI, 1996-200886/20.  
 XX  
 XX  
 PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.  
 XX  
 PS Example 1; Figure 1; 88pp; English.  
 XX  
 CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 67.8%; Score 61; DB 17; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 NVYLEKKWGA 16  
 |||||  
 DB 1 NVYLEKKWGA 11  
 |||||  
 RESULT 6  
 AAW43458  
 ID AAW43458 standard; peptide; 16 AA.  
 XX  
 AC AAW43458;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).  
 XX  
 KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.  
 XX  
 OS Synthetic.  
 OS Mycobacteria sp.  
 PN WO9711966-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 PI Elson CJ, Thompson JS;  
 XX  
 DR WPI, 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study

CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro.  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

XX Sequence 16 AA;

Query Match 67.8%; Score 61; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVVLEKRWGAP 16  
 |||||  
 1 NVVLEKRWGAP 11

RESULT 7

AAW434778 AAW434778 standard; peptide; 16 AA.

XX AAW434778;

XX 11-NOV-1996 (first entry)

DE Peptide from library spanning whole of hsp65.

KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.

OS Synthetic.

PN W09610039-A1.

PD 04-APR-1996.

PF 27-SEP-1995; 95WO-GB02295.

PR 27-SEP-1994; 94GB-0019553.

PA (2EPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;

XX WPI; 1996-200886/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC AAW4773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAW4772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.

XX Sequence 16 AA;

Query Match 63.3%; Score 57; DB 17; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0062;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEK 11  
 |||||  
 6 GPKGRNVVLEK 16

RESULT 8

AAW43456 AAW43456 standard; peptide; 16 AA.

XX AAW43456;

XX 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #6).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.

OS Synthetic.

OS Mycobacteria sp.

PN W09711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (2EPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

XX WPI; 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful  
 for treatment of autoimmune disease esp. arthritis  
 PS Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro.  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

XX Sequence 16 AA;

Query Match 63.3%; Score 57; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0062;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEK 11  
 |||||  
 6 GPKGRNVVLEK 16

RESULT 9

AAW43330 AAW43330 standard; peptide; 16 AA.

XX AAW43330;

XX 04-SEP-2000 (first entry)  
 DT Amino acid sequence of an epitope of heat shock protein 60.  
 DE Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 XX inflammatory disorder; arthritis.  
 KM Mycobacterium tuberculosis.  
 XX WO200027870-A1.  
 PN 18-MAY-2000.  
 PD 04-NOV-1999; 99WO-IL00595.  
 PF 05-NOV-1998; 98US-0107213.  
 PR (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX Naparstek Y, Ulmansky R, Kashi Y;  
 PI MPI; 2000-376486/32.  
 DR Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -  
 XX Claim 3; Page 7; 58pp; English.  
 PS The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX Sequence 16 AA;  
 SQ  
 QY Query Match 61.1%; Score 55; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 7 VVLEKKWGAP 16  
 1 VVLEKKWGAP 10  
 RESULT 10  
 AAU99965  
 ID AAU99965 standard; Peptide; 16 AA.  
 XX AAU99965;  
 AC 07-OCT-2002 (first entry)  
 DT Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.  
 DE Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 XX autoimmune disease; infectious disease; graft rejection; type I diabetes;  
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 XX arteriosclerosis.  
 XX Mycobacterium tuberculosis.  
 OS WO200248312-A2.  
 PN 20-JUN-2002.  
 PD 11-DEC-2001; 2001MO-IL01144.  
 PF 11-DEC-2000; 2000IL-0140233.  
 PR

XX (PEPT-) PEPTOR LTD.  
 PA Elias D, Avron A, Senderowitz H;  
 PI MPI; 2002-557613/59.  
 DR New backbone cyclized peptide analog of heat shock protein useful in  
 PT the treatment of e.g. autoimmune disease -  
 XX Claim 5; Page 42; 50pp; English.  
 PS The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.  
 XX Sequence 16 AA;  
 SQ  
 QY Query Match 61.1%; Score 55; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 7 VVLEKKWGAP 16  
 1 VVLEKKWGAP 10  
 RESULT 11  
 AAB88272  
 ID AAB88272 standard; Peptide; 11 AA.  
 XX AAB88272;  
 AC 17-MAY-2001 (first entry)  
 DT Hsp-65 peptide epitope #46.  
 DE Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;  
 XX immune response inducer; vaccine; gene therapy; bacterial infection;  
 KM tuberculosis.  
 XX Mycobacterium sp.  
 OS WO200116174-A2.  
 PN 08-MAR-2001.  
 PD 30-AUG-2000; 2000WO-IB01326.  
 PF 30-AUG-1999; 99US-0151396.  
 PR (KTES/) KTESLING R.  
 PA (CHAR/) CHARO J M.  
 PA (OTEN/) OTENHOFF T H M.  
 PA (GELU/) GELUK A.  
 XX Ktesling R, Charo JM, Otenhoff THM, Geluk A;  
 PI MPI; 2001-244396/25.  
 DR Novel polypeptides containing epitopes derived from Mycobacterial heat  
 XX shock protein 65 useful for treating bacterial and parasitic  
 PT infections, such as tuberculosis -  
 XX Disclosure; Page 55; 117pp; English.  
 PS The present sequence is a peptide epitope derived from Mycobacterial heat  
 CC

CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic  
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.  
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;  
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;  
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;  
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella  
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;  
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;  
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope  
 CC is useful for treating bacterial and parasitic infections such as  
 CC tuberculosis.  
 CC  
 SQ Sequence 11 AA;

Query Match 52.2%; Score 47; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVL 9  
 DB 3 GPKGRNVVL 11

RESULT 12  
 AAB88269  
 ID AAB88269 standard; Peptide; 10 AA.

AC AAB88269;

XX 17-MAY-2001. (first entry)

DE Hsp-65 peptide epitope #43.

XX Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;  
 KW immune response inducer; vaccine; gene therapy; bacterial infection;  
 KM tuberculosis.

XX Mycobacterium sp.

XX WO200116174-A2.

XX 08-MAR-2001.

PF 30-AUG-2000; 2000WO-IB01326.

XX 30-AUG-1999; 99US-0151396.

PA (KIES/) KIESSLING R.

PA (CHAR/) CHARO J M.

PA (OTEN/) OTENHOFF T H M.

PA (GELU/) GELUK A.

PI Kieselring R, Charo JM, Otenhoff TM, Geluk A;

DR WPI; 2001-244396/25.

XX Novel polypeptides containing epitopes derived from Mycobacterial heat  
 PT shock protein 65 useful for treating bacterial and parasitic  
 PT infections, such as tuberculosis -  
 XX  
 PS Disclosure; Page 55; 117pp; English.

XX The present sequence is a peptide epitope derived from Mycobacterial heat  
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic  
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.  
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;  
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;  
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;  
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella  
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;  
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;  
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope  
 CC is useful for treating bacterial and parasitic infections such as

CC tuberculosis.  
 XX Sequence 10 AA;

Query Match 47.8%; Score 43; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNV 8  
 DB 3 GPKGRNV 10

RESULT 13  
 AAB88279  
 ID AAB88279 standard; Peptide; 9 AA.

AC AAB88279;

XX 17-MAY-2001 (first entry)

DE Hsp-65 peptide epitope #53.

XX Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;  
 KW immune response inducer; vaccine; gene therapy; bacterial infection;  
 KM tuberculosis.

XX Mycobacterium sp.

XX WO200116174-A2.

XX 08-MAR-2001.

PF 30-AUG-2000; 2000WO-IB01326.

XX 30-AUG-1999; 99US-0151396.

PA (KIES/) KIESSLING R.

PA (CHAR/) CHARO J M.

PA (OTEN/) OTENHOFF T H M.

PA (GELU/) GELUK A.

PI Kieselring R, Charo JM, Otenhoff TM, Geluk A;

DR WPI; 2001-244396/25.

XX Novel polypeptides containing epitopes derived from Mycobacterial heat  
 PT shock protein 65 useful for treating bacterial and parasitic  
 PT infections, such as tuberculosis -  
 XX  
 PS Disclosure; Page 55; 117pp; English.

XX The present sequence is a peptide epitope derived from Mycobacterial heat  
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic  
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.  
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;  
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;  
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;  
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella  
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;  
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;  
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope  
 CC is useful for treating bacterial and parasitic infections such as  
 CC tuberculosis.

XX Sequence 9 AA;

Query Match 43.3%; Score 39; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNV 7  
 |||||

Db 3 GPKGRNV 9

RESULT 14

AAW434781  
ID AAR94781 standard; peptide; 15 AA.

XX AAR94781;

XX 11-NOV-1996 (first entry)

XX Peptide from library spanning whole of hsp65.

XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
KW prophylaxis.

XX Synthetic.

XX WO9610039-A1.

XX 04-APR-1996.

XX 27-SEP-1995; 95WO-GB02295.

XX 27-SEP-1994; 94GB-0019553.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Elson CJ, Thompson SJ;

XX WPI; 1996-200888/20.

XX Polypeptide derived from bacterial heat shock protein 65 - for use  
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
PT rheumatoid arthritis.

XX Example 1; Figure 1; 88pp; English.

XX AAR94773-R94878 are overlapping peptides of a library spanning the  
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65  
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as rheumatoid arthritis.

XX Sequence 15 AA;

Query Match 42.2%; Score 38; DB 17; Length 15;

Best Local Similarity 100.0%; Pred. NO. 12; Mismatches 0; Indels 0; Gaps 0;

QY 11 KKWGAP 16  
Db 1 KKWGAP 6

RESULT 15

AAW43459  
ID AAW43459 standard; peptide; 15 AA.

XX AAW43459;

XX 08-APR-1998 (first entry)

XX Mycobacteria sp. hsp68 derived peptide (group 1 #9).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
KW pristane induced arthritis; PIA.

XX Synthetic.  
OS Mycobacteria sp.

XX WO9711966-A1.

XX 03-APR-1997.

XX 26-SEP-1996; 96WO-GB02382.

XX 27-SEP-1995; 95GB-0019737.

XX (PEPT-) PEPTIDE THERAPEUTIC LTD.

XX Elson CJ, Thompson SJ;

XX WPI; 1997-212851/19.

XX Polypeptide(s) derived from microbial heat shock protein - useful  
PT for treatment of autoimmune disease esp. arthritis

XX Disclosure; Fig 1a; 91pp; English.

XX This peptide is one of a library (see AAW43451-W43556) which represents  
CC the mycobacterial heat shock protein, hsp65 and is designed to study  
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
CC arthritis. This fragment has been allocated as a group 1 peptide which  
CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
CC hsp65 is known to be an immunodominant antigen in a number of infectious  
CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
CC however heat shock proteins and peptides derived from microbial sources  
CC may act as self antigens and thus have limited clinical use. The human  
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
CC (see AAW43458-W4350) may be useful in the development of vaccines for  
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
CC arthritis.

XX Sequence 15 AA;

Query Match 42.2%; Score 38; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. NO. 12; Mismatches 0; Indels 0; Gaps 0;

QY 11 KKWGAP 16  
Db 1 KKWGAP 6

Search completed: December 30, 2003, 16:31:43  
Job time: 36 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:33:07 ; Search time 24.5 Seconds  
(without alignments)  
129.971 Million cell updates/sec

Title: US-09-847-637b-2  
Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 133148

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTIS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	16	US-09-847-637b-2	Sequence 2, Appli
2	55	61.1	16	US-09-847-637b-3	Sequence 3, Appli
3	34	37.8	14	US-09-848-664-3	Sequence 3, Appli
4	34	37.8	14	US-10-323-046-12	Sequence 12, Appli
5	34	37.8	14	US-10-405-339-5	Sequence 5, Appli
6	34	37.8	14	US-10-297-329-56	Sequence 56, Appli
7	34	37.8	14	US-10-106-804b-10	Sequence 10, Appli
8	31	34.4	13	US-09-852-455-68	Sequence 68, Appli
9	30	33.3	14	US-09-805-301-80	Sequence 80, Appli
10	29.5	32.8	16	US-10-161-791-228	Sequence 228, App
11	29.5	32.8	16	US-10-225-567A-1359	Sequence 1359, Ap
12	29	32.2	15	US-09-976-674-61	Sequence 61, Appli
13	29	32.2	15	US-10-194-441A-16	Sequence 16, Appli
14	29	32.2	15	US-10-194-441A-18	Sequence 18, Appli
15	28.5	31.7	10	US-09-572-404B-1036	Sequence 1036, Ap

16	28	31.1	12	US-10-185-050-184	Sequence 184, App
17	28	31.1	15	US-10-138-195-16	Sequence 16, Appli
18	27	30.0	8	US-09-984-056-58	Sequence 58, Appli
19	27	30.0	8	US-09-984-056-59	Sequence 59, Appli
20	27	30.0	8	US-09-984-057-58	Sequence 58, Appli
21	27	30.0	8	US-09-984-057-59	Sequence 59, Appli
22	27	30.0	8	US-10-105-232-58	Sequence 58, Appli
23	27	30.0	8	US-10-105-232-59	Sequence 59, Appli
24	27	30.0	8	US-10-189-437-58	Sequence 58, Appli
25	27	30.0	8	US-10-189-437-59	Sequence 59, Appli
26	27	30.0	14	US-09-824-438-20	Sequence 20, Appli
27	27	30.0	14	US-10-125-869A-97	Sequence 97, Appli
28	27	30.0	14	US-10-125-869A-103	Sequence 103, App
29	26	28.9	8	US-09-765-527-237	Sequence 237, App
30	26	28.9	9	US-09-732-411-6	Sequence 6, Appli
31	26	28.9	9	US-09-866-510-32	Sequence 32, Appli
32	26	28.9	9	US-10-091-724-8	Sequence 8, Appli
33	26	28.9	10	US-10-237-852-78	Sequence 78, Appli
34	26	28.9	12	US-10-119-528-100	Sequence 100, App
35	25.5	28.3	15	US-10-283-423-181	Sequence 181, App
36	25.5	28.3	15	US-10-213-821-181	Sequence 181, App
37	25	27.8	6	US-09-828-272A-7	Sequence 7, Appli
38	25	27.8	6	US-10-426-647-7	Sequence 7, Appli
39	25	27.8	6	US-10-193-709-15	Sequence 15, Appli
40	25	27.8	6	US-10-235-682-7	Sequence 7, Appli
41	25	27.8	7	US-10-300-699-46	Sequence 46, Appli
42	25	27.8	7	US-10-213-742-10	Sequence 10, Appli
43	25	27.8	8	US-09-828-272A-3	Sequence 3, Appli
44	25	27.8	8	US-10-426-647-3	Sequence 3, Appli
45	25	27.8	8	US-10-297-229-35	Sequence 35, Appli

#### ALIGNMENTS

RESULT 1  
US-09-847-637b-2  
Sequence 2, Application US/09847637B  
Patent No. US20020150586A1  
GENERAL INFORMATION:  
APPLICANT: Naparsky, Yaakov  
APPLICANT: Ulanovsky, Rita  
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
FILE REFERENCE: 13125-002001  
CURRENT APPLICATION NUMBER: US/09/847,637B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: PCT/IL99/00595  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,213  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 2  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-847-637b-2

Query Match 100.0%; Score 90; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKMGAP 16  
|||||  
Db 1 GPKGRNVVLEKKMGAP 16

RESULT 2  
US-09-847-637b-3  
Sequence 3, Application US/09847637B

Patent No. US20020150586A1  
GENERAL INFORMATION:  
APPLICANT: Napatsek, Yaakov  
APPLICANT: Umaneky, Rina  
APPLICANT: Kash, Vechekel  
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
FILE REFERENCE: 13125-002001  
CURRENT APPLICATION NUMBER: US/09/847, 637B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: PCT/IL99/00595  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,213  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-847-637B-3

Query Match 61.1%; Score 55; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLEKKWGAP 16  
Db 1 VLEKKWGAP 10

RESULT 3  
US-09-848-664-3  
Sequence 3, Application US/09848664  
Patent No. US2002014641A1  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbell, Jeffrey A.  
TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth  
TITLE OF INVENTION: Factors from Heparin Containing Matrices  
FILE REFERENCE: ETH 108  
CURRENT APPLICATION NUMBER: US/09/848, 664  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/298,084  
PRIOR FILING DATE: 1999-04-22  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-664-3

Query Match 37.8%; Score 34; DB 10; Length 14;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11  
Db 3 KGRNVLEK 11

RESULT 4  
US-10-323-046-12  
Sequence 12, Application US/10323046  
Publication No. US20030187232A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schenke, Jason C.  
APPLICANT: Sakiyama-Elbert, Shelly E.  
TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue  
TITLE OF INVENTION: Engineering

FILE REFERENCE: ETH 107 CIP (2)  
CURRENT APPLICATION NUMBER: US/10/323,046  
CURRENT FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: 09/141,153  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 12  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Heparin-binding sequence  
US-10-323-046-12

Query Match 37.8%; Score 34; DB 12; Length 14;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11  
Db 3 KGRNVLEK 11

RESULT 5  
US-10-405-339-5  
Sequence 5, Application US/10405339  
Publication No. US20030190364A1  
GENERAL INFORMATION:  
APPLICANT: Panitch, Alyssa  
APPLICANT: Seal, Brandon  
TITLE OF INVENTION: Biological Affinity Based Delivery Systems  
FILE REFERENCE: 9138-0079US  
CURRENT APPLICATION NUMBER: US/10/405,339  
CURRENT FILING DATE: 2003-04-01  
PRIOR APPLICATION NUMBER: US 60/369,568  
PRIOR FILING DATE: 2002-04-01  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-10-405-339-5

Query Match 37.8%; Score 34; DB 12; Length 14;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11  
Db 3 KGRNVLEK 11

RESULT 6  
US-10-297-229-56  
Sequence 56, Application US/10297229  
Publication No. US20030220245A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schoenmakers, Ronald  
TITLE OF INVENTION: CONJUGATE ADDITION REACTIONS FOR THE  
TITLE OF INVENTION: CONTROLLED DELIVERY OF PHARMACEUTICALLY ACTIVE COMPOUNDS  
FILE REFERENCE: 50154/003002  
CURRENT APPLICATION NUMBER: US/10/297,229  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: PCT/US01/18101  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: US 09/586,937



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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:30:27 ; Search time 14 Seconds

(Without alignments)  
48.355 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRVVLKRWGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 133293

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	40.0	8	2	US-08-467-822-11
2	36	40.0	8	3	US-08-432-697-11
3	36	40.0	8	3	US-08-466-248-11
4	34	37.8	14	4	US-09-675-922-12
5	30	33.3	9	4	US-09-289-942A-5
6	30	33.3	14	4	US-08-584-043A-80
7	30	33.3	16	3	US-08-602-999A-228
8	30	33.3	16	4	US-09-500-124-228
9	29.5	32.8	15	4	US-09-020-846-38
10	29	32.2	13	5	PCT-US95-07543-3
11	28	31.1	16	1	US-08-300-386A-38
12	28	31.1	16	5	US-08-931-645-38
13	28	31.1	16	5	PCT-US94-01258-38
14	28	31.1	16	5	PCT-US95-11235-38
15	27	30.0	9	1	US-08-452-083-23
16	27	30.0	9	1	US-08-468-557-12
17	27	30.0	10	2	US-08-556-597-158
18	27	30.0	14	4	US-09-217-228-20
19	27	30.0	15	3	US-08-491-954-9
20	26	28.9	6	1	US-08-076-032-56
21	26	28.9	6	2	US-08-730-486-56
22	26	28.9	7	1	US-08-076-092-53
23	26	28.9	7	1	US-08-730-486-53
24	26	28.9	8	1	US-08-076-092-49
25	26	28.9	8	2	US-08-672-610A-48
26	26	28.9	8	2	US-08-621-803-237
27	26	28.9	8	2	US-08-621-259A-239

28	26	28.9	8	2	US-08-621-259A-243	Sequence 243, App
29	26	28.9	8	2	US-08-730-486-49	Sequence 49, Appl
30	26	28.9	8	3	US-09-296-284-14	Sequence 14, Appl
31	26	28.9	8	3	US-09-217-352-237	Sequence 237, Appl
32	26	28.9	9	1	US-08-076-092-42	Sequence 42, Appl
33	26	28.9	9	2	US-08-730-486-42	Sequence 42, Appl
34	26	28.9	9	3	US-09-188-579-109	Sequence 109, App
35	26	28.9	9	3	US-09-315-444-109	Sequence 109, App
36	26	28.9	9	4	US-09-721-362-109	Sequence 109, App
37	26	28.9	10	3	US-08-159-339A-812	Sequence 812, App
38	26	28.9	11	6	5248606-34	Patent No. 5248606
39	26	28.9	12	1	US-07-778-233B-36	Sequence 36, Appl
40	26	28.9	12	1	US-07-963-321-36	Sequence 36, Appl
41	26	28.9	12	1	US-08-290-641-36	Sequence 36, Appl
42	26	28.9	12	1	US-08-330-599-10	Sequence 10, Appl
43	26	28.9	12	1	US-08-546-540-36	Sequence 36, Appl
44	26	28.9	12	2	US-08-726-306A-156	Sequence 156, App
45	26	28.9	12	5	PCT-US96-09809-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-08-467-822-11  
; Sequence 11, Application US/08467822  
; Patent No. 5843460  
; GENERAL INFORMATION:  
; APPLICANT: Labigne, Agnes  
; APPLICANT: Sauterbaum, Sebastien  
; APPLICANT: Ferrero, Richard L.  
; APPLICANT: Thibierge, Jean-Michel  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
; TITLE OF INVENTION: HERICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467, 822  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/432,697  
; FILING DATE: 02-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495, 0137-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-467-822-11

Query Match  
Best Local Similarity 40.0%; Score 36; DB 2; Length 8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7  
Db 2 GPKGRNV 8

RESULT 2  
US-08-432-697-11  
Sequence 11, Application US/08432697  
Patent No. 6248330

GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS: 44  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-432-697-11

Query Match  
Best Local Similarity 40.0%; Score 36; DB 3; Length 8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7  
Db 2 GPKGRNV 8

RESULT 3  
US-08-466-248-11  
Sequence 11, Application US/08466248

Patent No. 6258359  
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS: 44  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-248-11

Query Match  
Best Local Similarity 40.0%; Score 36; DB 3; Length 8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7  
Db 2 GPKGRNV 8

RESULT 4  
US-09-675-922-12  
Sequence 12, Application US/09675922  
Patent No. 6468731

GENERAL INFORMATION:  
APPLICANT: Hubbell A., Jeffrey  
APPLICANT: Schenke C., Jason  
APPLICANT: Sakiyama E., Shelley  
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue  
FILE REFERENCE: ETH 107 DIV  
CURRENT APPLICATION NUMBER: US/09/675,922

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:06 ; Search time 13.5 Seconds  
(without alignments)

113.978 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VVLEKMGAPRTTNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76.\*

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	25	28.7	13	1	MTMHAD
4	24	27.6	14	2	154945
5	22	25.3	8	2	A31570
6	22	25.3	13	2	G83988
7	21	24.1	11	2	S09074
8	21	24.1	13	2	A32734
9	21	24.1	13	2	A66126
10	21	24.1	14	2	S03530
11	21	24.1	15	2	S10388
12	21	24.1	16	2	PS0383
13	21	24.1	16	2	S26746
14	21	24.1	16	2	E28027
15	21	24.1	16	2	I37452
16	20	23.0	10	2	S42282
17	20	23.0	13	2	S47371
18	20	23.0	13	2	PH0928
19	20	23.0	13	4	I70076
20	20	23.0	14	2	S13864
21	20	23.0	14	2	A59018
22	20	23.0	15	2	S26791
23	20	23.0	15	2	S29386
24	20	23.0	15	2	T46625
25	20	23.0	15	2	A56970
26	20	23.0	15	2	S10386
27	20	23.0	16	1	MTDFBS
28	20	23.0	16	2	S03532
29	20	23.0	16	2	D49021

30	20	23.0	16	2	PH0749	T-cell receptor be
31	19	21.8	9	2	B38740	Ig kappa chain C r
32	19	21.8	10	1	XAV168	angiotensin-conver
33	19	21.8	10	2	PH1344	Ig heavy chain DJ
34	19	21.8	10	2	F33932	Ig mu chain J regi
35	19	21.8	11	2	PH1343	Ig heavy chain DJ
36	19	21.8	12	2	PH1324	Ig heavy chain DJ
37	19	21.8	13	2	S04014	lignin peroxidase
38	19	21.8	13	2	S57567	T cell receptor V-
39	19	21.8	13	2	A32486	beta protein - rat
40	19	21.8	13	2	I51905	collecting duct wa
41	19	21.8	14	2	PS0249	porin - rice (Sera
42	19	21.8	14	2	PT0223	Ig heavy chain CDR
43	19	21.8	14	2	PH1356	Ig heavy chain DJ
44	19	21.8	14	2	PH1332	Ig heavy chain DJ
45	19	21.8	15	2	S21241	oligo-1,6-glucosid

#### ALIGNMENTS

RESULT 1  
PH1631  
Ig H chain V-D-J region (Clone B-less 202) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1631  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1631  
A/Molecule type: DNA  
A/Residues: 1-15 <LEV>  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 29.9%; Score 26; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 5e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PTITNDG 16  
DB 4 PMVTTDG 10

#### RESULT 2

MTCMAD  
melanotropin alpha - Arabian camel  
C/Species: Camelus dromedarius (Arabian camel)  
C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998  
C/Accession: A01464  
R/Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.  
Biochemistry 14, 947-952, 1975  
A>Title: Isolation, characterization, and amino acid sequence of melanotropins from cam  
A/Reference number: A90393; MUID:75146434; PMID:1125179  
A/Accession: A01464  
A/Molecule type: protein  
A/Residues: 1-13 <LIC>  
C/Superfamily: corticotropin-lipotropin  
C/Keywords: acetylated amino end; blocked carboxyl end; hormone; pituitary  
F.1/Modified site: acetylated amino end (Ser) (partial) #status experimental  
F.13/Modified site: blocked carboxyl end (Val) (probably undated) #status experimental

Query Match 28.7%; Score 25; DB 1; Length 13;  
Best Local Similarity 60.0%; Pred. No. 6.3e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 RWGAP 10  
DB 8 RWGAP 12

## RESULT 3

MTHOAD

melanotropin alpha - horse

C/Species: Equus caballus (domestic horse)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C/Accession: A91785; A01464

R/Dixon, U.S.; Li, C.H.

J. Am. Chem. Soc. 82, 4568-4572, 1960

A/Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse

A/Reference number: A91785

A/Accession: A91785

A/Molecule type: protein

A/Residues: 1-13 &lt;DIX&gt;

C/Superfamily: corticotropin-11potropin

C/Keywords: blocked amino end; blocked carboxyl end; hormone; pituitary

F1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

F13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

## Query Match

28.7%; Score 25; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 6.3e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KMGAP 10

DB 8 RMGKP 12

## RESULT 4

154945 gene C protein - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999

C/Accession: 154945

R/Tao, T.; Bourne, J.C.; Blumenthal, R.M.

J. Bacteriol. 173, 1367-1375, 1991

A/Title: A family of regulatory genes associated with type II restriction-modification

A/Reference number: 154945; PMID:1995588

A/Accession: 154945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-14 &lt;RBS&gt;

A/Cross-references: GB:M63619; NID:g147664; PIDN:AAA2455.1; PID:g147665

## Query Match

27.6%; Score 24; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 1e+03;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKK 6

DB 4 VIMEKK 9

## RESULT 5

A31570 angiotensin-converting enzyme inhibitor - yellowfin tuna

C/Species: Thunnus albacares (yellowfin tuna)

C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000

C/Accession: A31570

R/Kohama, Y.; Matsunoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A/Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A/Reference number: A31570; MUID:88326322; PMID:3415688

A/Accession: A31570

A/Molecule type: protein

A/Residues: 1-8 &lt;KOH&gt;

A/Note: the source is designated as Neothunnus macropterus

C/Superfamily: unassigned animal peptides

C/Keywords: angiotensin-converting enzyme inhibitor

## Query Match

25.3%; Score 22; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KMG 8

DB 5 KMG 7

## RESULT 6

G83988 hypothetical protein BH2711 (imported) - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C/Accession: G83988

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hix

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: G83988

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 &lt;STO&gt;

A/Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06430.1; GSPDB:GNC

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH2711

Query Match 25.3%; Score 22; DB 2; Length 13;

Best Local Similarity 27.3%; Pred. No. 2e+03;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VLEKMGAPTI 12

DB 1 MIQKRSKPMI 11

## RESULT 7

809074 cytochrome P450-4b - rat (fragment)

N/Alternate names: cytochrome P450K-5

N/Contains: oxidoreductase (EC 1.-.-.-)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999

C/Accession: 809074

R/Imaoka, S.; Terano, Y.; Runae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A/Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with star

A/Reference number: 809072; MUID:90210577; PMID:2321956

A/Accession: 809074

A/Molecule type: protein

A/Residues: 1-11 &lt;IMA&gt;

C/Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C/Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 24.1%; Score 21; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 2.5e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PTTINDG 16

DB 4 PTXSLDG 10

## RESULT 8

A32734 enkephalin precursor - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 21-Jan-2000

C/Accession: A32734

R/Micanovic, R.; Ray, P.; Krugel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984

A/Title: Purification and sequence of an opioid peptide derived from ovine proenkephal:

A/Reference number: A32734; MUID:84128045; PMID:6546517

A/Accession: A32734

A/Status: preliminary

A/Molecule type: protein

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:26:11 ; Search time 10 Seconds  
(without alignments)

75.243 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VLEKKWGAPITNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 872

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.7	13	1	MIA_ANOCA
2	25	28.7	13	1	MIA_CAMDR
3	25	28.7	13	1	UNOI_PINS
4	23	26.4	11	1	ASL2_BACSE
5	22	25.3	8	1	ACI_THUAL
6	22	25.3	10	1	UNH3_HUMAN
7	20	23.0	13	1	UNO2_PINS
8	20	23.0	14	1	MCRX_METTM
9	20	23.0	16	1	MIB_SQUAC
10	19	21.8	10	1	BPP2_BOTJA
11	19	21.8	12	1	UP01_CAEEL
12	19	21.8	13	1	LIGB_TRAVE
13	19	21.8	14	1	SAP2_ARPRU
14	18	20.7	8	1	RT34_BOVIN
15	18	20.7	10	1	BPP2_BOTJA
16	18	20.7	10	1	BPP8_BOTIN
17	18	20.7	10	1	BPP_VIPAS
18	18	20.7	12	1	PSB3_PHYPA
19	18	20.7	13	1	LIGA_TRAVE
20	18	20.7	13	1	PSBP_PINS
21	18	20.7	13	1	TY13_PHYRO
22	18	20.7	15	1	MAL7_BACTO
23	17.5	20.1	5	1	BPP7_BOTIN
24	17	19.5	6	1	CBP2_MYTED
25	17	19.5	6	1	LOK1_LOCHI
26	17	19.5	8	1	LCK1_LEUMA
27	17	19.5	8	1	LCK2_LEUMA
28	17	19.5	8	1	LCK3_LEUMA
29	17	19.5	8	1	LCK4_LEUMA
30	17	19.5	8	1	LCK5_LEUMA
31	17	19.5	8	1	LCK6_LEUMA
32	17	19.5	8	1	LCK7_LEUMA
33	17	19.5	8	1	LCK8_LEUMA

34	17	19.5	9	1	PAR5_ASCSU	P43170	ascaris suu
35	17	19.5	10	1	PAR6_PANRE	P82660	panagrellus
36	17	19.5	10	1	HTF1_ROMMI	P18110	romalea mic
37	17	19.5	10	1	HTF2_CARMO	P11385	carausius m
38	17	19.5	10	1	HTF_HELZE	P16353	heliothis z
39	17	19.5	10	1	HTF_NAUCI	P10939	nauphoeta c
40	17	19.5	10	1	HTF_TABAT	P14596	tabanus atr
41	17	19.5	10	1	LBA5_JATMU	P13270	jatropha mu
42	17	19.5	10	1	LPK2_LOCHI	P41488	locusta mig
43	17	19.5	10	1	UPA9_HUMAN	P30095	homo sapien
44	17	19.5	12	1	H2AX_ONCMY	P83327	oncorhynch
45	17	19.5	13	1	IDHP_RAT	P56574	rattus norv

## ALIGNMENTS

```

RESULT 1
MIA_ANOCA          STANDARD;          PRT;          13 AA.
AC  P41589;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DS  Melanotropin alpha (Alpha-MSH).
DE  Melanotropin alpha (Green anole) (American chameleon).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX  NCBI_TaxID=28377;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Pituitary; PubMed=1667689;
RX  MEDLINE=92270473;
RA  Doses R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT  Isolation of a novel sequence change in the major form of alpha-MSH
RT  isolated from the intermediate pituitary of the reptile, Anolis
RL  Peptides 12:1261-1266(1991).
CC  -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR  InterPro: IPR001941; Mcoitin ACTH.
DR  Pfam: PF00976; ACTH_domain; I.
KM  Hormone; Amidation.
FT  MOD RES 13
FT  SEQUENCE 13 AA; 1608 MW; FF990A7358B09C1 CRC64;
SQ
Query Match          28.7%; Score 25; DB 1; Length 13;
Best local similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY  6 KWGAP 10
DB  8 RMGKP 12

RESULT 2
MIA_CAMDR          STANDARD;          PRT;          13 AA.
AC  P01198;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DS  Melanotropin alpha (Alpha-MSH).
DE  Melanotropin alpha (Dromedary) (Arabian camel), and
OS  Equus caballus (Horse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX  NCBI_TaxID=9838, 9796;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=C. dromedarius;
RX  MEDLINE=75146434; PubMed=1125179;
RA  Li C.H., Danto W.O., Chung D., Rao A.J.;
RT  Isolation, characterization, and amino acid sequence of

```

```

RESULT 4
ASL2_BACSE
ID _ASL2_BACSE STANDARD; PRT; 11 AA.
AC P8147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfatase lysase 2 (EC 4.2.2.-) (Fragment).
OC Bacteroides stercoris.
OC Bacteriaria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HU-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfatase, two
RT novel heparinases, from Bacteroides stercoris HU-15."
RL Eur. J. Biochem. 268:2635-2641 (2001).
CC -1- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -1- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -1- SUBUNIT: Monomer.
CC -1- PTM: The N-terminus is blocked.
CC -1- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 26.4%; Score 23; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

GY 13 TNDG 16
|||
Db 5 TNDG 8

RESULT 5
ACT_THUVAL
ID _ACT_THUVAL STANDARD; PRT; 8 AA.
AC P16691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacora (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acenthomorphii; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle."
RL Biochem. Biophys. Res. Commun. 155:332-337 (1988).
DR PIR. A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 25.3%; Score 22; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:41 ; Search time 28 Seconds

(without alignments)  
147.459 Million cell updates/sec

Title: US-09-847-637B-3  
Perfect score: 87  
Sequence: 1 VVLEKMGAPRTTNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4022

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.7	10	11	070580 mus musculus
2	25	28.7	16	2	045530 O45530 bacillus su
3	25	28.7	16	4	09UCR9 O9UCR9 homo sapien
4	23	27.6	14	2	047599 O47599 escherichia
5	23	26.4	11	15	083410 O83410 mouse mamma
6	23	26.4	13	15	085645 O85645 mouse mamma
7	23	26.4	16	2	010748 O10748 clostridium
8	23	26.4	16	4	09UCR8 O9UCR8 homo sapien
9	23	26.4	16	10	09S8D6 O9S8D6 triticum ae
10	22	25.3	12	15	098240 O98240 human immun
11	22	25.3	13	16	09K9D7 O9K9D7 bacillus ha
12	22	25.3	15	8	099386 O99386 sus scrofa
13	21	24.1	8	8	094PX5 O94PX5 felis silve
14	21	24.1	8	8	094VB2 O94VB2 varanus sal
15	21	24.1	8	8	094PX7 O94PX7 felis silve
16	21	24.1	8	8	094PX6 O94PX6 felis libyc

17	21	24.1	8	8	094VA7 O94VA7 varanus sal
18	21	24.1	8	8	094VB5 O94VB5 varanus sal
19	21	24.1	8	9	08SB0 O8SB0 bacterioph
20	21	24.1	8	9	08H9K1 O8H9K1 bacterioph
21	21	24.1	9	8	094VC6 O94VC6 varanus pil
22	21	24.1	10	8	094VD5 O94VD5 varanus pil
23	21	24.1	12	13	08AUP8 O8AUP8 salmo trutt
24	21	24.1	13	8	09MQX0 O9MQX0 cervus elap
25	21	24.1	13	8	09MQK6 O9MQK6 rupicapra r
26	21	24.1	13	8	09MQK3 O9MQK3 capra ibex
27	21	24.1	13	16	08XAF5 O8XAF5 escherichia
28	21	24.1	14	12	P91578 P91578 choristomou
29	21	24.1	15	4	09BXK4 O9BXK4 homo sapien
30	21	24.1	15	8	P92076 P92076 euhadra her
31	21	24.1	16	4	Q14495 Q14495 homo sapien
32	21	24.1	16	5	Q9NFW0 Q9NFW0 trypanosoma
33	20	23.0	11	2	Q9EUZ3 Q9EUZ3 escherichia
34	20	23.0	11	15	08ADI8 O8ADI8 human immun
35	20	23.0	12	15	08QDY5 O8QDY5 human immun
36	20	23.0	12	15	08Q347 O8Q347 human immun
37	20	23.0	12	15	08QDY4 O8QDY4 human immun
38	20	23.0	12	15	08Q341 O8Q341 human immun
39	20	23.0	12	15	08Q345 O8Q345 human immun
40	20	23.0	12	15	08Q343 O8Q343 human immun
41	20	23.0	12	15	08QDY6 O8QDY6 human immun
42	20	23.0	13	1	Q50831 Q50831 methanococc
43	20	23.0	13	4	Q14462 Q14462 homo sapien
44	20	23.0	15	6	Q9TS39 Q9TS39 gorilla gor
45	20	23.0	15	10	Q9S914 Q9S914 hordeum vul

## ALIGNMENTS

## RESULT 1

ID 070580 PRELIMINARY; PRT; 10 AA.  
AC 070580;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Carbonic anhydrase III (Fragment).  
GN CAR3 OR CAR3 OR CAR3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sowden J., Smith H., Morrison K., Edwards Y.;  
RT "Sequence comparisons and functional studies of the proximal promoter  
of the carbonic anhydrase 3 (CA3) gene."  
RL Gene 214:157-165(1999)  
DR EMBL; AJ006474; CAA07057.1; -  
DR MGD; MGI:88270; Car3.  
DR MGD; MGI:1351477; Car3.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1105 MW; 56F7BE71ADC37B13 CRC64;

Query Match 28.7%; Score 25; DB 11; Length 10;  
Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEKKWAP 10  
DB 1 MAKEWATP 8

RESULT 2  
ID 045530 PRELIMINARY; PRT; 16 AA.  
AC 045530;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Chloramphenicol acetyltransferase (EC 2.3.1.28) (Fragment).  
 GN CAT.  
 OS Bacillus subtilis.  
 OC Bacterias; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NC NCB1\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M168; TRANSPOSON=TN9;  
 RX MEDLINE=85113144; PubMed=2982142;  
 RA Lin C.K., Goldfarb D.S., Doi R.H., Rodriguez R.L.;  
 RT "Mutations that affect the translation efficiency of Tn9-derived cat  
 gene in Bacillus subtilis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:173-177 (1985).  
 CC -1- FUNCTION: THIS ENZYME IS AN EFFECTOR OF CHLORAMPHENICOL RESISTANCE  
 IN BACTERIA.  
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + CHLORAMPHENICOL = COA +  
 CHLORAMPHENICOL 3-ACETATE.  
 CC -1- SIMILARITY: BELONGS TO THE CHLORAMPHENICOL ACETYLTRANSFERASE  
 FAMILY.  
 CC EMBL; M12657; AAA22291.1; -  
 DR Acetyltransferase; Antibiotic resistance; Transferase.  
 FT NON TER 16 16 B4894C04C5A5409F CRC64;  
 SQ SEQUENCE 16 AA; 1936 MW; B4894C04C5A5409F CRC64;  
  
 QY Query Match 28.7%; Score 25; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEKKGAPTI 12  
 DB 1 MEKKIGYTV 10  
  
 RESULT 3  
 Q9UCK9 PRELIMINARY; PRT; 16 AA.  
 AC Q9UCK9;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
 DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)  
 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93099171; PubMed=1463770;  
 RA Baba S., Takahashi T., Kasama T., Shiraawa H.;  
 RT "Identification of two novel amyloid A protein subsets coexisting in  
 an individual patient of AA-amyloidosis."  
 RL Biochim. Biophys. Acta 1180:195-200 (1992).  
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
 COMPLEX (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
 SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.  
 DR InterPro; IPR000096; Serum amyloid\_A.  
 DR Pfam; PF00277; SAA\_proteins; 1.  
 KM Acute phase; HDL.  
 SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;  
  
 QY Query Match 28.7%; Score 25; DB 4; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 WGAPTTN 14  
 DB 7 WAAEVISN 14

RESULT 4  
 ID Q47599 PRELIMINARY; PRT; 14 AA.  
 AC Q47599;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE C (Fragment).  
 GN C.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NC NCB1\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139577; PubMed=1995588;  
 RA Tao T., Bourne J.C., Blumenthal R.M.;  
 RT "A family of regulatory genes associated with type II restriction-  
 modification systems."  
 RL J. Bacteriol. 173:1367-1375 (1991).  
 DR EMBL; M63619; AAA24555.1; -  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1705 MW; 77B6CA60581A4F3B CRC64;  
  
 QY Query Match 27.6%; Score 24; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLEKK 6  
 DB 4 VVLEKK 9

RESULT 5  
 ID Q83410 PRELIMINARY; PRT; 11 AA.  
 AC Q83410;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Superantigen (Fragment).  
 GN SAg.  
 OS Mouse mammary tumor virus.  
 OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.  
 NC NCB1\_TaxID=11757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mtv-6;  
 RX MEDLINE=95133174; PubMed=7831795;  
 RA Cho K., Patrick D.A., Morris D.W.;  
 RT "Structure and biological activity of the subgenomic Mtv-6 endogenous  
 provirus."  
 RL Virology 206:395-402 (1995).  
 DR EMBL; U37518; AA66863.1; -  
 DR InterPro; IPR001213; MMTV\_SAg.  
 DR Pfam; PF01054; MMTV\_SAg; 1.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326CD7 CRC64;

QY Query Match 26.4%; Score 23; DB 15; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEKXW 7  
 DB 4 LQOKW 8

RESULT 6  
 ID Q85645 PRELIMINARY; PRT; 13 AA.  
 AC Q85645;



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# OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:36 ; Search time 35 Seconds  
(without alignments)  
72.561 Million cell updates/sec

Title: US-09-847-637B-3  
Sequence: 1 VLEKMGAPITINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 360314

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1960.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1961.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1962.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1963.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1964.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1965.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1966.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1967.DAT:*
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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1971.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1972.DAT:*
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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1979.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	16	AA193330	Amino acid sequenc
2	87	100.0	16	AAU99965	Mycobacterium tube
3	81	93.1	16	AAW43458	Mycobacterium sp. h
4	76	87.4	16	AAW434780	Peptide from libra
5	70	80.5	15	AAW43459	Mycobacteria sp. h
6	65	74.7	15	AAW4781	Peptide from libra
7	55	63.2	16	AAU99329	Amino acid sequenc
8	55	63.2	16	AAU99964	Mycobacterium tube
9	48	55.2	15	AAW4779	Peptide from libra

10	48	55.2	15	18	AAW43457
11	39	44.8	15	23	AAW26843
12	39	44.8	16	16	AAW43460
13	35	40.2	16	16	AAW87908
14	35	40.2	16	17	AAW10516
15	34	39.1	16	17	AAW94782
16	32	36.8	12	23	AAW6064
17	31.5	36.2	16	23	AAU83423
18	31.5	36.2	16	23	AAU83424
19	31.5	36.2	16	23	AAU83425
20	31	35.6	12	22	AAU90858
21	31	35.6	12	24	ABG74642
22	31	35.6	15	12	AAW14808
23	31	35.6	15	20	AAW34136
24	31	35.6	15	21	AAW52607
25	31	35.6	15	21	AAW52607
26	30	34.5	10	21	AAW32456
27	30	34.5	10	21	AAW54380
28	30	34.5	12	22	AAW08829
29	30	34.5	14	18	AAW38766
30	30	34.5	14	18	AAW24451
31	30	34.5	15	23	ABG61615
32	30	34.5	16	14	AAW32709
33	30	34.5	16	18	AAW25443
34	29	33.3	7	23	ABU04516
35	29	33.3	9	22	AAW45892
36	29	33.3	13	23	ABB97728
37	29	33.3	13	23	ABB97729
38	28	32.2	9	19	AAW56753
39	28	32.2	12	18	AAW38002
40	28	32.2	13	23	AAW40804
41	28	32.2	13	24	AAE34758
42	28	32.2	14	22	AAW00664
43	28	32.2	14	24	AAW026122
44	28	32.2	15	19	AAW37382
45	28	32.2	15	23	ABG96155

## ALIGNMENTS

RESULT 1	AAW93330	standard; peptide; 16 AA.
ID	AAW93330;	
AC	AAW93330;	
DT	04-SEP-2000 (first entry)	
DE	Amino acid sequence of an epitope of heat shock protein 60.	
KW	Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease; inflammatory disorder; arthritis.	
OS	Mycobacterium tuberculosis.	
PN	WO200027870-A1.	
PD	18-MAY-2000.	
PF	04-NOV-1999; 99WO-IL00595.	
PR	05-NOV-1998; 98US-0107213.	
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.	
PI	Naparetek Y, Umaneky R, Kaehi Y;	
DR	WPI, 2000-376486/32.	
PT	Peptide having a defined sequence is used in vaccines for conferring immunity against autoimmune disease or inflammatory disorders, especially arthritis -	

Mycobacteria sp. h  
Arabidopsis thaliana  
Mycobacteria sp. h  
Bovine lactoferrin  
Lactoferrin derivative  
Peptide from libra  
Human glucocerebro  
Bacterial fructosyl  
Bacterial fructosyl  
Melanocyte stimula  
C. unshiu FUS pept  
fcs oncogene prote  
Variant human pote  
v-fes encoded onco  
fcs-encoded oncop  
Human secreted pro  
Amino acid sequenc  
Human scavenger re  
Delivery peptide u  
Nucleic acid (NA)  
Human DPRP-3 pepti  
N terminal of haem  
Gtb2 N-terminal SH  
Molt-4 leukemia c  
Human tumor-associ  
Human procathepsin  
Human procathepsin  
A. tumefaciens ant  
KW domain binding  
Te-1 binding surz  
Streptomyces sp. s  
Human protein frag  
Fc region binding  
Hepatitis C virus  
Cysteine-containin

XX Claim 3; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTNDG 16  
 DB 1 VLEKKKGAPTTNDG 16

# RESULT 2

ID AAW99965 standard; Peptide; 16 AA.

AC AAW99965;

DT 07-OCT-2002 (first entry)

DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.

XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
 KM autoimmune disease; infectious disease; graft rejection; type I diabetes;  
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
 KM arteriosclerosis.

XX Mycobacterium tuberculosis.

PN WO200248312-A2.

PD 20-JUN-2002.

PF 11-DEC-2001; 2001WO-IL01144.

PR 11-DEC-2000; 2000IL-0140233.

XX (PEPT-) PEPTOR LTD.

PI Elias D, Avron A, Senderowitz H;

DR WPI; 2002-557613/59.

XX New backbone cyclised peptide analog of heat shock protein useful in  
 PT the treatment of e.g. autoimmune disease -

PS Claim 5; Page 42; 50pp; English.

XX The invention relates to backbone cyclised peptide analogues or  
 CC antagonists of heat shock protein (hsp). The analogues and antagonists  
 CC are useful in the treatment of chronic inflammatory disease, autoimmune  
 CC disease, infectious disease and graft rejection, and for diagnosing  
 CC autoimmune and inflammatory disease including juvenile rheumatoid  
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus  
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide  
 CC analogue of a heat shock protein.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTNDG 16  
 DB 1 VLEKKKGAPTTNDG 16

# RESULT 3

ID AAW43458 standard; peptide; 16 AA.

AC AAW43458;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.

XX Synthetic.

OS Mycobacteria sp.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

XX (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI; 1997-212851/19.

XX Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91pp; English.

XX This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW44948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

XX Sequence 16 AA;

Query Match 93.1%; Score 81; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTND 15  
 DB 2 VLEKKKGAPTTND 16

# RESULT 4

ID AAR94780 standard; peptide; 16 AA.

AC AAR94780;

XX

DT 11-NOV-1996 (first entry)  
 XX Peptide from library spanning whole of hsp65.  
 DE Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.  
 XX Synthetic.  
 OS  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1996-200888/20.  
 XX  
 PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.  
 XX  
 PS Example 1; Figure 1; 88pp; English.  
 XX  
 CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides concy. This sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 87.4%; Score 76; DB 17; Length 16;  
 Best Local Similarity 93.3%; Pred. No. 3.2e-06;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VVEKKKGAPTTND 15  
 DB 2 VVEKKKGAPTTND 16  
 RESULT 5  
 AAM43459  
 ID AAM43459 standard; peptide; 15 AA.  
 XX  
 AC AAM43459;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).  
 XX  
 KM Heat shock protein; hsp68; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.  
 XX  
 OS Synthetic.  
 OS Mycobacteria sp.  
 XX  
 PN WO9711966-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.

XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAM43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAM14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.5%; Score 70; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KKGAPTTNDG 16  
 DB 1 KKGAPTTNDG 12  
 RESULT 6  
 AAR94781  
 ID AAR94781 standard; peptide; 15 AA.  
 XX  
 AC AAR94781;  
 XX  
 DT 11-NOV-1996 (first entry)  
 XX  
 DE Peptide from library spanning whole of hsp65.  
 XX  
 KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI; 1996-200888/20.  
 XX  
 PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.  
 XX

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the  
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65  
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as rheumatoid arthritis.

XX Sequence 15 AA;

Query Match 74.7%; Score 65; DB 17; Length 15;  
Best Local Similarity 91.7%; Pred. No. 0.00023;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KKWGAPTTNDG 16  
DB 1 KKWGAPTTNDG 12

RESULT 7  
AAY93329  
ID AAY93329 standard; peptide; 16 AA.

XX AAY93329;

DT 04-SEP-2000 (first entry)

XX Amino acid sequence of an epitope of heat shock protein 60.

XX Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX inflammatory disorder; arthritis.

XX Mycobacterium tuberculosis.

XX WO200027870-A1.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-IL00595.

XX 05-NOV-1998; 98US-0107213.

XX (HADA-) HADAST MEDICAL RES SERVICES & DEV.

XX Naparstek Y, Ulmansky R, Kashi Y;

XX WPI; 2000-376486/32.

XX Peptide having a defined sequence is used in vaccines for conferring  
XX immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis -

XX Claim 2; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
XX 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
XX nucleic acid encoding it, are useful in vaccines for conferring  
XX immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis. The peptide may also be used to raise  
XX antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match 63.2%; Score 55; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKWGAP 10  
DB 1 VLEKKWGAP 10

DB 7 VLEKKWGAP 16

RESULT 8  
AAU99964  
ID AAU99964 standard; Peptide; 16 AA.

XX AAU99964;

DT 07-OCT-2002 (first entry)

XX Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.

XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;  
XX autoimmune disease; infectious disease; graft rejection; type I diabetes;  
XX juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;  
XX systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.  
XX arteriosclerosis.

XX Mycobacterium tuberculosis.

XX WO200248312-A2.

XX 20-JUN-2002.

XX 11-DEC-2001; 2001WO-IL01144.

XX 11-DEC-2000; 2000IL-0140233.

XX (PEPT-) PEPTOR LTD.

XX Elias D, Avron A, Senderowitz H;

XX WPI; 2002-557613/59.

XX New backbone cyclized peptide analog of heat shock protein useful in  
XX the treatment of e.g. autoimmune disease -

XX Claim 5; Page 42; 50pp; English.

XX The invention relates to backbone cyclised peptide analogues or  
XX antagonists of heat shock protein (hsp). The analogues and antagonists  
XX are useful in the treatment of chronic inflammatory disease, autoimmune  
XX disease, infectious disease and graft rejection, and for diagnosing  
XX autoimmune and inflammatory disease including juvenile rheumatoid  
XX arthritis, type I diabetes, multiple sclerosis, systemic lupus  
XX erythematosus, inflammatory bowel disease, uveitis, thyroiditis and  
XX arteriosclerosis. This sequence represents a backbone cyclised peptide  
XX analogue of a heat shock protein.

XX Sequence 16 AA;

Query Match 63.2%; Score 55; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKWGAP 10  
DB 7 VLEKKWGAP 16

RESULT 9  
AAR94779  
ID AAR94779 standard; peptide; 15 AA.

XX AAR94779;

DT 11-NOV-1996 (first entry)

XX Peptide from library spanning whole of hsp65.

XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;

XX prophylaxis.  
 XX Synthetic.  
 XX WO9610039-A1.  
 XX PD 04-APR-1996.  
 XX PF 27-SEP-1995; 95WO-GB02295.  
 XX PR 27-SEP-1994; 94GB-0019553.  
 XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX PI Elson CJ, Thompson SJ;  
 XX WPI, 1996-200888/20.  
 XX PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.  
 XX PS Example 1; Figure 1; 88pp; English.  
 XX CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.  
 XX SQ Sequence 15 AA;  
 XX  
 XX Query Match 55.2%; Score 48; DB 17; Length 15;  
 XX Best Local Similarity 100.0%; Pred. No. 0.2;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEKKWGA 9  
 Db 7 VLEKKWGA 15  
 XX  
 XX RESULT 10  
 XX AAW43457  
 XX ID AAW43457 standard; peptide; 15 AA.  
 XX AC AAW43457;  
 XX DT 08-APR-1998 (first entry)  
 XX DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).  
 XX KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristane induced arthritis; PIA.  
 XX OS Synthetic.  
 XX OS Mycobacteria sp.  
 XX PN WO9711966-A1.  
 XX PD 03-APR-1997.  
 XX PF 26-SEP-1996; 96WO-GB02382.  
 XX PR 27-SEP-1995; 95GB-0019737.  
 XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX PI Elson CJ, Thompson SJ;

XX WPI, 1997-212851/19.  
 XX PT Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis  
 XX PS Disclosure; Fig 1a; 91pp; English.  
 XX CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW1948-W1950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 XX SQ Sequence 15 AA;  
 XX  
 XX Query Match 55.2%; Score 48; DB 18; Length 15;  
 XX Best Local Similarity 100.0%; Pred. No. 0.2;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEKKWGA 9  
 Db 7 VLEKKWGA 15  
 XX  
 XX RESULT 11  
 XX AAE26843  
 XX ID AAE26843 standard; peptide; 15 AA.  
 XX AC AAE26843;  
 XX DT 13-DEC-2002 (first entry)  
 XX DE Anabaena variabilis peptide #16 having tocopherol cyclase activity.  
 XX KM Tocopherol cyclase; 2, 3-dimethylphytylquinol cyclase; tocol; tocopherol;  
 KM tocotrienol; food; feed; vitamin E; enzyme.  
 XX OS Anabaena variabilis.  
 XX PN WO200263016-A1.  
 XX PD 15-AUG-2002.  
 XX PF 30-JAN-2002; 2002WO-EP00973.  
 XX PR 02-FEB-2001; 2001EP-0102397.  
 XX PA (HOPE) ROCHE VITAMINS AG.  
 XX PI Chougnet A, Friedlein AM, Woggon W;  
 XX WPI, 2002-666954/71.  
 XX PT Novel tocopherol cyclase protein, useful for the biotechnological  
 PT production of vitamin E for use in producing food or feed compositions  
 XX  
 XX Example 4; Page 31; 61pp; English.  
 XX The present invention relates to novel tocopherol cyclase (2, 3-dimethyl-  
 CC phytylquinol cyclase) proteins and their corresponding polynucleotides.  
 CC Tocopherol cyclase proteins catalyse the reaction of 2, 3-dimethyl-5-  
 CC phytyl-1,4-benzoquinol to RRR-gamma-tocopherol. They are involved in the  
 CC biosynthetic production of tocols, tocopherols or tocotrienols. They are

CC also useful for the production of a food or feed composition comprising  
CC vitamin E. The present sequence is Anabaena variabilis peptide having  
CC tocopherol cyclase activity.

CC Sequence 15 AA;

Query Match 44.8%; Score 39; DB 23; Length 15;  
Best Local Similarity 70.0%; Pred. No. 7.2;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 WCAPITINDG 16  
:|||||  
DB 1 FGAPQIVNDG 10

RESULT 12  
AAM43460  
ID AAM43460 standard; peptide; 16 AA.

AC AAM43460;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #10).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
XX rheumatoid arthritis; antigen; infectious disease; propylactic;  
XX pristanic induced arthritis; PIA.

OS Synthetic.  
OS Mycobacteria sp.

PN WC9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI; 1997-212851/19.

XX Polypeptide(s) derived from microbial heat shock protein - useful  
PT for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91p; English.

CC This peptide is one of a library (see AAM43451-WA3556) which represents  
CC the mycobacterial heat shock protein, hsp65 and is designed to study  
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
CC arthritis. This fragment has been allocated as a group 1 peptide which  
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial  
CC hsp65 is known to be an immunodominant antigen in a number of infectious  
CC diseases and is linked to pristanic induced arthritis (PIA) in vitro,  
CC however heat shock proteins and peptides derived from microbial sources  
CC may act as self antigens and thus have limited clinical use. The human  
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
CC (see AAM14948-W14950) may be useful in the development of vaccines for  
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
CC arthritis.

CC Sequence 16 AA;

Query Match 44.8%; Score 39; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PTTINDG 16  
|||||||

DB 1 PTTINDG 7

RESULT 13  
AAR87908

ID AAR87908 standard; peptide; 16 AA.

AC AAR87908;

DT 01-MAR-1996 (first entry)

DE Bovine lactoferrin (24-39).

XX antiviral; lactoferrin;

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "optionally this site is acetylated or  
preceded by a peptide"

FT Modified-site 16 /note= "optionally this site may be in amide form  
or followed by a peptide"

PN JP07069915-A.

PD 14-MAR-1995.

PF 02-SEP-1993; 93JP-0240284.

PR 02-SEP-1993; 93JP-0240284.

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

DR WPI; 1995-144726/19.

XX Inhibitor against viral infection and proliferation - contains  
PT peptide having sequence from lactoferrin

PS Claim 4; Page 2; 10pp; Japanese.

CC The sequence is one of six peptides disclosed as having inhibitory  
CC effect against viral infection. The peptides are derived from  
CC lactoferrin. Their activity is demonstrated against cytomegalovirus.

CC Sequence 16 AA;

Query Match 40.2%; Score 35; DB 16; Length 16;  
Best Local Similarity 77.8%; Pred. No. 38;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KKWGAPRIT 13  
|||||  
DB 4 KKGAPRIT 12

RESULT 14

ID AAM10516 standard; peptide; 16 AA.

AC AAM10516;

DT 02-APR-1997 (first entry)

DE Lactoferrin derived antibacterial peptide.

XX Lactoferrin; antibacterial; immunogen; monoclonal; antibody;  
XX human; bovine; hybridoma; sensitive; specific; detection;  
XX determination; gastric juice; intestine; faeces; blood; urine.

OS Synthetic.

```

PN      JF08269099-A.
XX
PD      15-OCT-1996.
XX
XX      30-MAR-1995; 95JP-00731177.
XX
XX      30-MAR-1995; 95JP-00731177.
XX
XX      (MORG ) MORINAGA MILK IND CO LTD.
XX
XX      WPI; 1996-515017/51.
XX
XX      Monoclonal antibody combined with bovine or non-natural human
PT      lactoferrin fragment - for detecting lactoferrin-originated
PT      antibacterial peptide in e.g. gastric juice, urine etc
XX
PS      Claim 3; Page 12; 13pp; Japanese.
XX
XX      The present peptide is a lactoferrin (LF) derived antibacterial
CC      peptide, which can be used as an immunogen in the prepn. of a
CC      monoclonal antibody (Mab), capable of binding with a human or
CC      bovine LF fragment but not with natural LF, using standard
CC      hybridoma techniques. The Mab can be used for the highly sensitive
CC      and specific detection or determination of LF derived antibacterial
CC      peptides in gastric juice, intestinal contents, faeces, blood and
CC      urine.
XX
SQ      Sequence 16 AA;

Query Match      40.2%; Score 35; DB 17; Length 16;
Best Local Similarity 77.8%; Pred. NO. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 KKWGAPRTT 13
        |||||
        2 KKGAPRST 10
DB
RESULT 15
AAR94782
ID      AAR94782 standard; peptide; 16 AA.
XX
AC      AAR94782;
XX
DT      11-NOV-1996 (first entry)
XX
DE      Peptide from library spanning whole of hsp65.
XX
XX      Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW      rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW      prophylaxis.
XX
XX      Synthetic.
XX
XX      WO9610039-A1.
XX
XX      04-APR-1996.
XX
XX      27-SEP-1995; 95WO-GB02295.
XX
XX      27-SEP-1994; 94GB-0019553.
XX
XX      (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX      Elson CJ, Thompson SJ;
XX
XX      WPI; 1996-200888/20.
XX
XX      Polypeptide derived from bacterial heat shock protein 65 - for use
PT      in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT      rheumatoid arthritis.
XX
PS      Example 1; Figure 1; 88pp; English.

```

```

XX
CC      AAR94773-R94878 are overlapping peptides of a library spanning the
CC      whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC      prepared from the library and used to immunise mice, after 10 days the
CC      mice received injections of pristane to induce arthritis and the
CC      animals examined for incidence of arthritis. A preferred anti-arthritis
CC      peptide was found to correspond to residues 21-31 of full length hsp65
CC      (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC      treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC      diseases such as rheumatoid arthritis.
XX
SQ      Sequence 16 AA;

Query Match      39.1%; Score 34; DB 17; Length 16;
Best Local Similarity 85.7%; Pred. NO. 57;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 PTTNDG 16
        |||||
        1 PTTNDG 7
DB

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Job time : 35 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:33:07 ; Search time 24.5 Seconds  
(without alignments)  
129.971 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VVLEKKMGAPITINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 133148

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	10	US-09-847-637B-3
2	55	63.2	16	10	US-09-847-637B-2
3	32	36.8	9	12	US-10-228-167A-3
4	32	36.8	12	10	US-09-753-126-100
5	32	36.8	12	11	US-09-896-896A-64
6	31.5	36.2	16	10	US-09-995-587A-33
7	31.5	36.2	16	10	US-09-995-587A-34
8	31.5	36.2	16	10	US-09-995-587A-35
9	31.5	36.2	16	10	US-09-995-587A-36
10	31	35.6	15	12	US-10-350-405-5
11	31	35.6	15	12	US-10-350-405-217
12	31	35.6	15	15	US-10-121-746-80
13	30	34.5	14	10	US-09-805-301-80
14	30	34.5	15	10	US-09-976-674-61
15	30	34.5	16	12	US-10-161-791-228

16	29	33.3	13	12	US-10-230-033-40	Sequence 40, Appl
17	28	32.2	12	15	US-10-185-050-184	Sequence 184, App
18	28	32.2	13	11	US-09-852-455-68	Sequence 68, Appl
19	28	32.2	13	15	US-10-145-415-65	Sequence 65, Appl
20	28	32.2	13	15	US-10-057-789-227	Sequence 227, App
21	28	32.2	13	15	US-10-212-628-227	Sequence 227, App
22	28	32.2	14	12	US-10-125-869A-102	Sequence 102, App
23	27	31.0	14	11	US-09-824-438-20	Sequence 20, Appl
24	27	31.0	14	12	US-10-195-730-253	Sequence 253, App
25	27	31.0	14	12	US-10-125-869A-97	Sequence 97, Appl
26	27	31.0	15	12	US-10-125-869A-103	Sequence 103, App
27	27	31.0	15	12	US-10-138-195-16	Sequence 16, Appl
28	26	29.9	8	9	US-09-765-527-237	Sequence 237, App
29	26	29.9	9	9	US-09-732-411-6	Sequence 6, Appl
30	26	29.9	9	10	US-09-866-510-32	Sequence 32, Appl
31	26	29.9	9	15	US-10-091-724-8	Sequence 8, Appl
32	26	29.9	10	12	US-10-237-852-78	Sequence 78, Appl
33	26	29.9	14	8	US-08-424-550B-455	Sequence 455, App
34	26	29.9	14	11	US-09-906-393A-3	Sequence 3, Appl
35	26	29.9	15	15	US-10-225-567A-1448	Sequence 1448, Ap
36	26	29.9	16	9	US-09-844-813-11	Sequence 11, Appl
37	26	29.9	16	12	US-10-031-874A-164	Sequence 164, App
38	25	28.7	6	10	US-09-828-272A-7	Sequence 7, Appl
39	25	28.7	6	12	US-10-426-647-7	Sequence 7, Appl
40	25	28.7	6	15	US-10-193-709-15	Sequence 15, Appl
41	25	28.7	6	15	US-10-235-682-7	Sequence 7, Appl
42	25	28.7	7	12	US-10-300-699-46	Sequence 46, Appl
43	25	28.7	7	12	US-10-213-742-10	Sequence 10, Appl
44	25	28.7	8	10	US-09-828-272A-3	Sequence 3, Appl
45	25	28.7	8	12	US-10-426-647-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-847-637B-3  
Sequence 3, Application US/09847637B  
Patent No. US20020150586A1  
GENERAL INFORMATION:  
APPLICANT: Naparstek, Yaakov  
APPLICANT: Ulanovsky, Rina  
APPLICANT: Kashl, Yecheskel  
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING  
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH  
FILE REFERENCE: 13125-002001  
CURRENT APPLICATION NUMBER: US/09/847, 637B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: PCT/IL99/00595  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107, 213  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-847-637B-3  
Query Match 100.0%; Score 87; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVLEKKMGAPITINDG 16  
DB 1 VVLEKKMGAPITINDG 16  
RESULT 2  
US-09-847-637B-2  
Sequence 2, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Napatstek, Yaakov
; APPLICANT: Ulimansky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-2

Query Match      63.2%; Score 55; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLEKKMGAP 10
Db      7 VLEKKMGAP 16

RESULT 3
US-10-228-167A-3
; Sequence 3, Application US/10228167A
; Publication No. US20030147909A1
; GENERAL INFORMATION:
; APPLICANT: Hernan Marshall Gonzalez, Sergio
; TITLE OF INVENTION: HIGHLY IMMUNOGENIC PROTEIN AGAINST THE INTRACELLULAR PATHOGEN AGH
; TITLE OF INVENTION: PISCIRICKETTSIA SALMONIS, WHICH AFFECTS SALMON CULTURE, AMINO AC
; TITLE OF INVENTION: ACID SEQUENCES OF SAID PROTEIN AND ITS APPLICATION IN THE DEVELO
; FILE REFERENCE: 076502-9004
; CURRENT APPLICATION NUMBER: US/10/228,167A
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: Chilean Patent Application No. US20030147909A1 2086-2001
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-228-167A-3

Query Match      36.8%; Score 32; DB 12; Length 9;
Best Local Similarity 85.7%; Pred. No. 6.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 WGAFTTT 13
Db      2 FGAFTTT 8

RESULT 4
US-09-753-126-100
; Sequence 100, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING

```

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; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-753-126-100

Query Match      36.8%; Score 32; DB 10; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 APTITND 15
Db      1 APTITND 7

RESULT 5
US-09-896-896A-64
; Sequence 64, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAYYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217us210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-896-896A-64

Query Match      36.8%; Score 32; DB 11; Length 12;

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 16:30:27 ; Search time 14 Seconds  
(without alignments)  
48.355 Million cell updates/sec

Title: US-09-847-637B-3  
Perfect score: 87  
Sequence: 1 VLEKKMGAPTINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 133293

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	36.8	10	3	US-08-687-590-67
2	31	35.6	9	4	US-09-289-942A-5
3	31	35.6	15	4	US-09-336-643A-70
4	30	34.5	14	4	US-08-584-043A-80
5	30	34.5	16	3	US-08-602-999A-228
6	30	34.5	16	3	US-08-030-410-1
7	30	34.5	16	4	US-09-500-124-228
8	28	32.2	15	4	US-09-020-846-38
9	27	31.0	7	3	US-08-687-590-72
10	27	31.0	9	1	US-08-452-083-23
11	27	31.0	9	1	US-08-468-557-12
12	27	31.0	10	2	US-08-556-597-158
13	27	31.0	14	4	US-09-217-228-20
14	27	31.0	15	1	US-07-907-190-8
15	27	31.0	15	1	US-08-320-373-37
16	27	31.0	15	3	US-08-491-954-9
17	26	29.9	6	3	US-08-893-654B-15
18	26	29.9	8	2	US-08-621-803-237
19	26	29.9	8	2	US-08-621-259A-239
20	26	29.9	8	2	US-08-621-259A-243
21	26	29.9	8	3	US-09-296-284-14
22	26	29.9	8	3	US-09-217-352-237
23	26	29.9	10	2	US-08-556-597-145
24	26	29.9	10	2	US-08-556-597-152
25	26	29.9	11	1	US-08-346-849-23
26	26	29.9	11	1	US-08-293-284A-23
27	26	29.9	11	4	US-08-898-300-23

28	26	29.9	11	6	5248606-34	Patent No. 5248606
29	26	29.9	12	1	US-07-778-223B-36	Sequence 36, App1
30	26	29.9	12	1	US-07-963-321-36	Sequence 36, App1
31	26	29.9	12	1	US-08-290-641-36	Sequence 36, App1
32	26	29.9	12	1	US-08-548-540-36	Sequence 36, App1
33	26	29.9	12	5	PCT-US96-09809-36	Sequence 36, App1
34	26	29.9	14	4	US-08-468-260A-455	Sequence 455, App
35	26	29.9	14	4	US-08-488-446-455	Sequence 455, App
36	26	29.9	14	4	US-08-467-344A-455	Sequence 455, App
37	26	29.9	15	1	US-08-111-939-10	Sequence 21, App1
38	26	29.9	16	1	US-08-307-724B-21	Sequence 21, App1
39	26	29.9	16	3	US-09-242-131A-11	Sequence 11, App1
40	26	29.9	16	4	US-09-615-283-11	Sequence 11, App1
41	25	28.7	6	3	US-08-472-595-6	Sequence 6, App1
42	25	28.7	6	3	US-08-207-575A-6	Sequence 6, App1
43	25	28.7	6	3	US-08-246-441-15	Sequence 15, App1
44	25	28.7	6	4	US-09-393-585-15	Sequence 15, App1
45	25	28.7	7	3	US-08-946-525-10	Sequence 10, App1

## ALIGNMENTS

RESULT 1  
US-08-687-590-67  
Sequence 67, Application US/08687590  
Patent No. 6255070  
GENERAL INFORMATION:  
APPLICANT: Willison, Keith Robert  
APPLICANT: Kubota, Hiroshi  
APPLICANT: Ashworth, Alan  
TITLE OF INVENTION: Folding Proteins  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,590  
FILING DATE: 31-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/00192  
FILING DATE: 31-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9401791.0  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9418234.2  
FILING DATE: 09-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Baerian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 084619-000000US  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-687-590-67  
Query Match 36.8%; Score 32; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 TITNDG 16  
Db 1 TITNDG 6

## RESULT 2

US-09-289-942A-5  
; Sequence 5, Application US/09289942A  
; Patent No. 6482928  
; GENERAL INFORMATION:  
; APPLICANT: Pat, Emil F.  
; APPLICANT: Klein, Michel H.  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Arthur  
; TITLE OF INVENTION: Fab'-EPITOPH COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5  
; FILE REFERENCE: 1038-926 MIS:jb  
; CURRENT APPLICATION NUMBER: US/09/289,942A  
; CURRENT FILING DATE: 1999-04-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-289-942A-5

Query Match 35.6%; Score 31; DB 4; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2.5e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 EKKMGAPT 11  
Db 2 EDKWDAPS 9

## RESULT 3

US-09-336-643A-70  
; Sequence 70, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Ruter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Primer  
US-09-336-643A-70

Query Match 35.6%; Score 31; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 WCAPTITNDG 16  
Db 1 TITNDG 1

Db 2 WGVVTTTIG 11

## RESULT 4

US-08-584-043A-80  
; Sequence 80, Application US/08584043A  
; Patent No. 6344436  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Sparrow, James T.  
; APPLICANT: Hauer, Joche  
; APPLICANT: Mims, Martha P.  
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
; TITLE OF INVENTION: MACROMOLECULE DELIVERY  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 6.0  
; SOFTWARE: Word Perfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,043A  
; FILING DATE: January 8, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 217/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-584-043A-80

Query Match 34.5%; Score 30; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LKKW 7  
Db 5 LKKW 9

## RESULT 5

US-08-602-999A-228  
; Sequence 228, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.